Heliyon 10 (2024) e24711

Contents lists available at ScienceDirect

Heliyon

journal homepage: www.cell.com/heliyon

Research article

Uncertain SEIAR system dynamics modeling for improved community health management of respiratory virus diseases: A COVID-19 case study

Mohammad Mahdi Ershadi [*], Zeinab Rahimi Rise

Department of Industrial Engineering and Management Systems, Amirkabir University of Technology, Tehran, Iran

A R T I C L E I N F O

Keywords:
Uncertain SEIAR
System dynamics
Respiratory virus outbreaks
Disease spread forecasting
Scenario analysis
COVID-19

A B S T R A C T

The study investigates the significance of employing advanced systemic models in community health management, with a focus on COVID-19 as a respiratory virus. Through the development of a system dynamics model integrating an uncertain SEIAR model, our research addresses the critical issue of parameter uncertainty using Ensemble Kalman Filter (EnKF) and Metropolis-Hastings (MH) algorithms. We present a case study using real COVID-19 outbreaks in Iran, offering insights into effective outbreak control scenarios and considering the global impact of respiratory viruses. The research yields distinctive results, showcasing variable mortality rates (40,500 to 436,500) across scenarios in Iran. Model accuracy is rigorously evaluated using the Normalized Root-Mean-Square Deviation (NRMSD) for new cases, deaths, and recoveries (0.2 %, 1.2 %, and 0.6 % respectively). The outcomes not only contribute to the existing body of knowledge but also offer practical implications for healthcare policies, economic considerations, and sensitivity assessments related to respiratory diseases. This study stands out from others in its approach to modeling and addressing uncertainty within a system dynamics framework. The integration of EnKF and MH algorithms provides a nuanced understanding of parameter uncertainty, adding a layer of sophistication to the analysis. The application of the model to real-world COVID-19 outbreaks in Iran further enhances the study's relevance and applicability. In conclusion, the research introduces an uncertain SEIAR system dynamics model with unique contributions to policymaking, economic considerations, and sensitivity assessments for respiratory diseases. The outcomes and insights derived from the study not only advance our understanding of disease dynamics but also provide actionable information for effective public health management.

1. Introduction

Respiratory viruses are widespread causes of human diseases globally, with notable types including ADV, HBoV, HCoV, HMPV, HPIV, HRSV, HRV, PCF, SARS, and SARS-CoV. A recent addition to this group is COVID-19, first identified in Wuhan in December 2019. Given the multifaceted factors influencing virus outbreaks, the situation is intricate and unpredictable. Developing models to understand epidemic dynamics is crucial for public health interventions. Among these, compartmental models like the SIR model are commonly used. However, SIR models fall short in representing all relevant aspects such as vaccination and effective subsystems.

* Corresponding author.
E-mail address: zeinab.rahimi@aut.ac.ir (M.M. Ershadi).

https://doi.org/10.1016/j.heliyon.2024.e24711
Received 27 August 2023; Received in revised form 10 January 2024; Accepted 12 January 2024
Available online 26 January 2024

Abbreviations

ADV	Adenovirus
EnKF	Ensemble Kalman Filter
HBoV	Human Bocavirus
HCoV	Human Coronavirus
HMPV	Human Metapneumovirus
HPIV	Human Parainfluenza Virus
HRSV	Human Respiratory Syncytial Virus
HRV	Human Rhinovirus
MH	Metropolis-Hastings
PCF	Pharyngoconjunctival Fever
SARS	Severe Acute Respiratory Syndrome
SARS-CoV	Coronavirus Associated with SARS
SEIAR	Susceptible, Exposed, Infectious, Asymptomatic, and Removed
SEIR	Susceptible, Exposed, Infectious, and Removed
SIR	Susceptible, Infectious, and Removed
MCMC	Markov chain Monte Carlo
RMAEs	Relative Mean Absolute Errors
NRMSD	Normalized Root Mean Square Deviation

These limitations, coupled with uncertainties due to changing environments and human behaviors, lead to inaccurate predictions. To address the challenges posed by nonlinear, diverse, and stochastic epidemic patterns, novel approaches are essential. This paper tackles these issues through parameter estimation and data assimilation techniques, reducing the disparity between predictions and real observations. Consequently, we propose a scenario-based system dynamics model to aid governments in managing and curtailing the spread of COVID-19, a significant respiratory virus.

Accurate parameter estimation is pivotal in enhancing epidemic models. Parameters vary based on geographic regions, reflecting differing epidemic spread patterns, demographics, and environmental dynamics. Moreover, model parameters evolve with the refinement of infectious disease models. Hence, previous parameter values lose relevance, demanding a redefinition aligned with local epidemic data and model structures. Widely employed parameter estimation methods include MCMC algorithms, particle swarm optimization, and iterative filtering methods. Furthermore, data assimilation plays a significant role in epidemic forecasting by merging direct and indirect observations from various sources into models, enhancing the realism of model trajectories.

In the context of respiratory virus diseases, including COVID-19, it is necessary to develop effective models and address parameter uncertainties and integrate real-world data. Through innovative approaches like data assimilation, we can enhance our understanding of epidemic dynamics and ultimately improve prediction accuracy.

2. Literature review

The extant literature on respiratory diseases reflects a rich tapestry of research, encompassing diverse methodologies that contribute substantially to our comprehension of disease dynamics, transmission patterns, and strategies for mitigation. Notably, a myriad of studies have delved into this domain, each bringing unique perspectives and approaches to the forefront.

Zuo et al. (2023) [1] significantly advanced our understanding by utilizing statistical models to assess the impact of non-pharmaceutical interventions on respiratory disease incidence during the COVID-19 pandemic in China. Their work provided valuable insights into the effectiveness of interventions during a public health crisis. In the realm of predictive modeling, Cui et al. (2022) [2] distinguished themselves by devising a microscopic-level model that surpassed existing macroscopic models in forecasting disease transmission trends with heightened accuracy. This underscores the importance of granular, detailed models for capturing the nuances of disease dynamics. Exploring a different facet, Guo et al. (2022) [3] investigated temperature-mortality associations and elucidated distinct vulnerabilities across age groups. Their work contributes to a holistic understanding of the multifaceted factors influencing respiratory diseases, highlighting the importance of considering demographic variables. Urban public transportation systems, as elucidated by Guo et al. (2023) [4], emerged as a crucial focal point in understanding disease spread. Their findings emphasize the necessity of preventive measures in such environments, offering practical implications for public health interventions. Arias et al. (2023) [5] leveraged machine learning for emergency health care demand predictions, demonstrating the versatility of advanced technologies in healthcare planning and resource allocation. Tasar et al. (2022) [6] achieved promising results in respiratory sound classification with a novel approach, showcasing the potential of innovative methods in disease diagnosis and monitoring. Jalasto et al. (2022) [7] delved into the intricate interplay of occupations, socioeconomic status, and respiratory diseases across different countries, providing a nuanced understanding of the social determinants influencing health outcomes. Estimating the impact of influenza on healthcare systems, Bernadou et al. (2023) [8] offered insights into the strain placed on hospital resources during disease outbreaks. He et al. (2023) [9] focused on the role of air pollution control in mitigating respiratory illnesses, contributing to the broader discourse on environmental factors affecting public health. Highlighting the intersection of climate and health, Krüger and Nedel (2022) [10]

Table 1
Research papers and their techniques and variables.

Num	Reviewed Topic	Reference	Year	Utilized Variables	Used Techniques	Used Subsystems	Case Study	Country
[1]	Trends in respiratory diseases before and after COVID-19	Zuo et al.	2023	Disease incidence	ARIMA, GLM	NPIs, respiratory	China	China
[2]	Forecasting transmission trends of respiratory diseases	Cui et al.	2022	Transmission trends	Microscopic model	Individual movement	United States	Global
[3]	Effects of daily temperature on mortality from respiratory diseases	Guo et al.	2022	Temperature, mortality	Nonlinear models	Temperature variations	Mianyang City	China
[4]	Dynamic model of disease transmission in urban transportation	Guo et al.	2023	Disease spread, public transportation	Dynamic model	Rail transit system	Small town	China
[5]	Predicting emergency health care demands due to respiratory diseases	Arias et al.	2023	Health care demands	Machine learning algorithms	Health emergency service	Jaeön city	Spain
[6]	Accurate respiratory sound classification model	Tasar et al.	2022	Sound classification	Piccolo pattern, classifiers	Biomedical signal processing	–	–
[7]	Occupation and socioeconomic status in chronic obstructive respiratory diseases	Jalasto et al.	2022	Occupation, socioeconomic status	Regression algorithms	Respiratory diseases	Finland, Estonia, Sweden	Europe
[8]	Burden of influenza-attributable severe acute respiratory infections	Bernadou et al.	2023	Hospitalizations, influenza	Data analysis, estimation	Hospitalization data	Metropolitan France	France
[9]	Optimal control of air pollution to reduce respiratory diseases	He et al.	2023	Air pollution, respiratory diseases	Deterministic, stochastic models	Respiratory diseases	–	–
[10]	Relationship between climate and hospital admissions	Krüger and Nedel	2022	Hospital admissions, climate	Correlation analysis	Hospital admissions	Brazil	Brazil
[11]	PM2.5 and SISP Respiratory Diseases	Shi, Qi	2022	PM2.5, SISP	Qualitative analysis	SISP dynamics	Air pollution effects	Not specified
[12]	Adaptive Interventions and Vaccination Strategies	Goldenbogen et al.	2022	NPIs, vaccination	Agent-based modeling	Community dynamics	Germany (Jan–Sep 2021)	Germany
[13]	Direct and Indirect Effects of Air Pollution on Diseases	Shi, Qi, Ding	2023	Direct/Indirect effects	Bifurcation analysis	Respiratory disease model	–	–
[14]	Longitudinal Audio Data for COVID-19 Progression Prediction	Dang et al.	2022	Audio biomarkers	Sequential deep learning	COVID-19 progression	–	–
[15]	COVID-19 and Influenza Transmission	Song et al.	2022	COVID-19, Influenza	Mathematical modeling	Disease transmission	Germany (2011–2021)	Germany
[16]	Quantifying Contact Patterns	Breen et al.	2022	Contact patterns	Multilevel regression	Disease spread	United States	United States
[17]	Mobility Restrictions and COVID-19 Spread	Fazio et al.	2022	Mobility restrictions	Agent-based modeling	COVID-19 spread	Italy	Italy
[18]	Contact Rates and Transmission	Ringa et al.	2022	Contact rates	Segmented regression	Disease transmission	British Columbia	Canada
[19]	Uncertain SEIAR Model for COVID-19 Cases	Jia and Chen	2021	Uncertain SEIAR	Epidemic modeling	COVID-19 cases	China	China
[20]	Asymptomatic Cohort in Epidemic Spread	Pribylová, Hajnova	2020	Asymptomatic cohort	Compartmental modeling	Disease spread	–	–

(continued on next page)

Table 1 (*continued*)

Num	Reviewed Topic	Reference	Year	Utilized Variables	Used Techniques	Used Subsystems	Case Study	Country
[21]	COVID-19 Spread with Population Migration	Chen et al.	2020	Infected and Basic Reproduction Numbers, Population Migration	SEIR Modeling, Intervention Analysis	Disease Spread, Population Movement	COVID-19 Pandemic	–
[22]	Urban Transportation and Disease Spread	Qian & Ukkusuri	2021	Mobility Dynamics, *Trans*-SEIR Model	Mathematical Modeling, Optimal Control	Urban Transportation, Disease Transmission	New York City	USA
[23]	ICU Admission Prediction in COVID-19	Sadat Asl et al.	2022	ICU Admission Prediction, Fuzzy Expert Systems	Fuzzy Logic, ANFIS	Medical Decision-Making	COVID-19 Patients	–
[24]	Health Workforce Planning Under Universal Health Coverage	Leerapan et al.	2021	Health Workforce Demand and Supply, System Dynamics Modeling	Group Model Building, Stock and Flow Diagrams	Healthcare Workforce Planning	Thailand	Thailand
[25]	Preventive Healthcare Facility Network Design	Ershadi & Shemirani	2021	Network Configuration, Client Choice, Resource Constraints	Mixed Integer Linear Programming, Genetic Algorithm	Healthcare Facility Network	Isfahan City	Iran
[26]	Diagnostics, Testing, and Contact Tracing for COVID-19	Fair et al.	2021	Epidemiology, Diagnostics, Testing, Contact Tracing	Systems Dynamics Modeling, Experimental Design	Epidemiological Systems	–	–
[27]	Vaccination-Resource Constraints	Zhang et al.	2020	Vaccination-Dependent Basic Reproduction Number, Resource Constraints	Lyapunov Functions, Optimal Control Theory	Vaccination Strategy	–	–
[28]	System Dynamics for Infectious Disease Modeling	Rubin et al.	2021	Infectious Disease Modeling, System Dynamics	Causal Loop Analysis, System Dynamics Modeling	Epidemic Models	–	–
[29]	Crisis Management Among Refugees	Allahi et al.	2021	Epidemic Crisis Response, System Dynamic Model	System Dynamics Modeling	Refugee Health and Education	Syrian Refugees in Turkey	Turkey
[30]	COVID-19 Prevention and Control Strategies	Jia et al.	2022	Prevention and Control Model, System Dynamics Analysis	System Dynamics Modeling	Disease Prevention and Control	–	–
[31]	COVID-19 infection dynamics	Hu et al.	2021	Infected people	System Dynamics Modeling	Wuhan, Hubei, China	China	China
[32]	Tourism recovery strategies post-COVID-19	Gu et al.	2022	Tourist behavior	Behavioral simulation	Small Island Developing States	Maldives	Various
[33]	Pandemic response policies	Sy et al.	2020	Infection, economy	System Dynamics Modeling	Disease transmission system	Various	Various
[34]	Policy innovation and health tech emergence	Aminullah & Erman	2021	Policy complexity	System Dynamics Modeling	Early COVID-19 handling in Indonesia	Indonesia	Indonesia
[35]	Fuzzy fractal control for pandemic control	Castillo & Melin	2021	Control concepts	Fuzzy fractal	COVID-19 pandemic	Global	Global
[36]	COVID-19 outbreak in Iran and its impact on transportation system	Rahimi Rise et al.	2020	Infected people, mortality rates, recovery rates	System dynamics modeling	Health care systems, transportation, public contact, capacity of food and drug networks	Iran	–
[37]	Socioeconomic analysis of infectious diseases based on different scenarios	Rise et al.	2022	Variables impacting infectious diseases, GDP prediction	Uncertain SEIAR model, ANFIS	Healthcare systems, transportation, contacts, capacities of food and pharmaceutical networks	–	–
[38]	Multidisciplinary analysis of international environments based	Rahimi Rise, Z. et al.	2022	Environmental considerations, global economy	Literature analysis	–	–	–

(*continued on next page*)

Table 1 (*continued*)

Num	Reviewed Topic	Reference	Year	Utilized Variables	Used Techniques	Used Subsystems	Case Study	Country
	on impacts of Covid-19			shift, public-health resilient systems				
[39]	Multi-objective optimization model for logistic planning in crisis response phase	Ershadi and Shemirani	2022	Types of injured people, vehicles, logistic planning	Multi-objective optimization, Lexicographic method	–	–	–
[40]	Comprehensive analysis of epidemic prevention measures	Zhu et al.	2023	Population dynamics	SEIAR model	Population mobility, vaccination, retesting	Hong Kong, Shenzhen	China

explored the interaction between climate and hospital admissions for respiratory diseases in Brazil during the COVID-19 pandemic, shedding light on the complex relationship between environmental factors and disease prevalence.

Air pollution's intricate connection to respiratory diseases has garnered substantial attention. Shi and Qi (2022) [11] proposed strategies to mitigate PM2.5 pollution, aligning air quality improvements with enhanced patient care. Goldenbogen et al. (2022) [12] underscored the necessity for adaptive interventions, considering community dynamics and vaccination strategies. Extending this analysis, Shi, Qi, and Ding (2023) [13] delved into the impact of air pollution on both direct and indirect disease transmission modes. COVID-19-specific research has demonstrated diverse perspectives. Dang et al. (2022) [14] showcased the potential of audio data in predicting COVID-19 progression through deep learning. Song et al. (2022) [15] emphasized non-pharmaceutical interventions' importance for both COVID-19 and influenza transmission. Breen et al. (2022) [16] quantified disease-relevant contact patterns, while Fazio et al. (2022) [17] assessed mobility restriction impacts through an agent-based approach. Ringa et al. (2022) [18] highlighted close-contact rates' significance in disease dynamics. Jia and Chen (2021) [19] introduced uncertainty into epidemic modeling, enhancing COVID-19 case predictions, and Pribylová and Hajnova (2020) [20] explored the role of asymptomatic cohorts in COVID-19 spread. Chen et al. (2020) [21] incorporated population migration into an extended SEIR model, revealing intervention strategies'

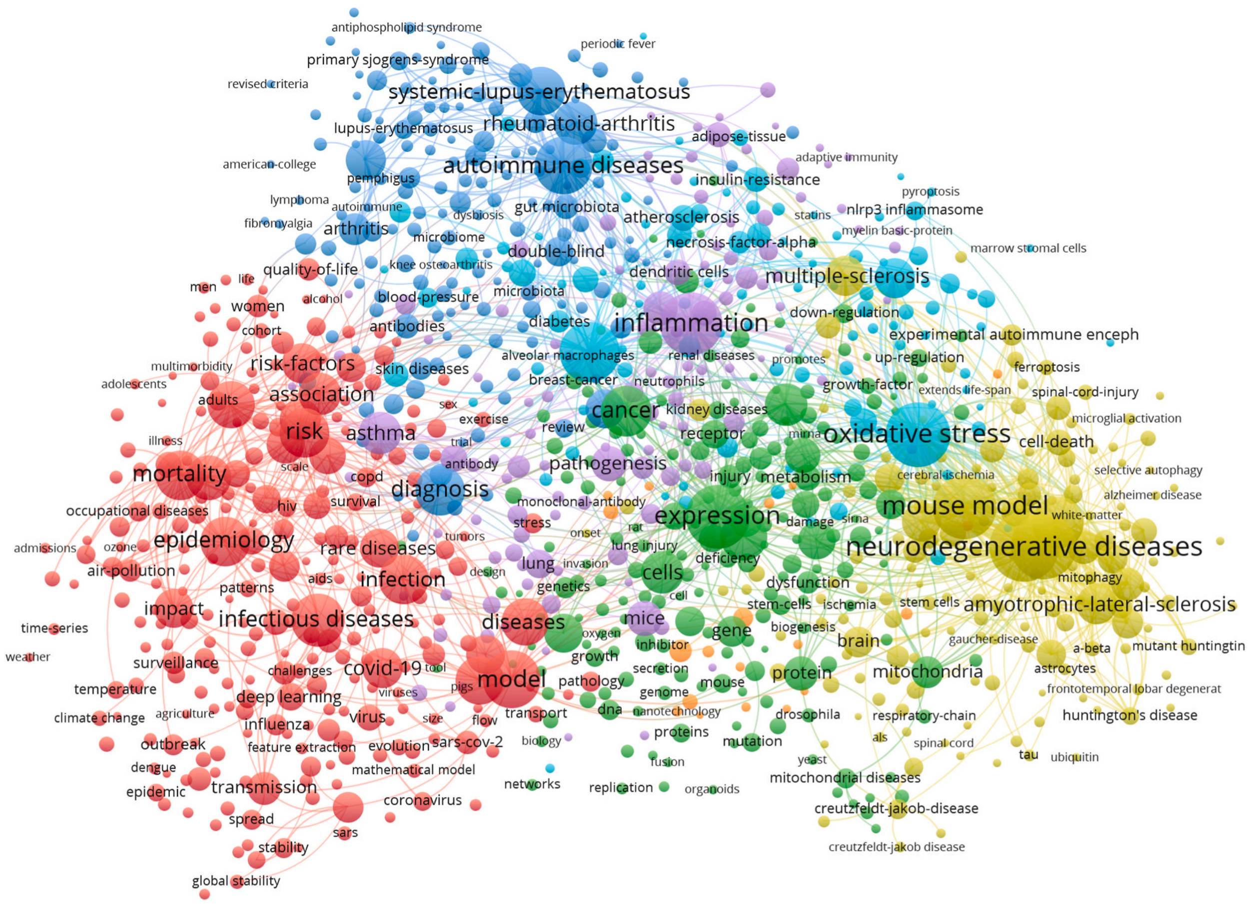

Fig. 1. A representation of map of science for various applications and research areas related to diseases in WoS.

impact.

Examining urban transportation's role in disease transmission, Qian and Ukkusuri (2021) [22] developed a *Trans*-SEIR model, illustrating the influence of mobility patterns. In medical decision-making, Sadat Asl et al. (2022) [23] used fuzzy expert systems for ICU admission predictions, and Leerapan et al. (2021) [24] employed system dynamics for healthcare workforce planning. Ershadi and Shemirani (2021) [25] focused on preventive healthcare facility network design, while Fair et al. (2021) [26] used interconnected system dynamics models to address uncertainties in COVID-19 diagnostics, testing, and contact tracing. Zhang et al. (2020) [27] optimized control strategies for a two-group epidemic model with vaccination-resource constraints. System dynamics models found utility in understanding infectious diseases more broadly. Rubin et al. (2021) [28] advocated for system dynamics' simplicity and effectiveness, and Allahi et al. (2021) [29] evaluated crisis management responses in refugee populations. Jia et al. (2022) [30] assessed COVID-19 prevention and control strategies, highlighting dynamic intervention effects. Hu et al. (2021) [31] estimated infected individuals in different regions of China using a multivariate Monte Carlo optimization approach. Gu et al. (2022) [32] examined tourism recovery strategies post-COVID-19 for Small Island Developing States. Sy et al. (2020) [33] recommended pandemic response policies by analyzing the interplay between disease transmission and economic impact. Aminullah and Erman (2021) [34] explored policy innovation and health technology emergence in COVID-19 handling in Indonesia.

In the realm of modeling for respiratory disease dynamics, Castillo and Melin (2021) [35] innovatively proposed a fuzzy fractal control approach tailored for nonlinear dynamic systems, with a practical application demonstrated in the context of COVID-19 control. Rahimi Rise et al. (2020) [36] delved into COVID-19 outbreak scenarios within Iran, emphasizing the pivotal role of the transportation system. Rise and Ershadi (2022) [37] and Rahimi et al. (2022) [38] extended their focus to the international impacts of COVID-19, advocating for institutional reforms to fortify public health systems globally. Ershadi and Shemirani (2022) [39] enriched the literature with a multi-objective optimization model designed for crisis response planning, encompassing considerations for injured individuals and logistical planning. In a recent contribution, Zhu et al. (2023) [40] introduced an SEIAR model specifically tailored to analyze the efficacy of multiple epidemic prevention measures for COVID-19. Their work underscored the importance of diverse strategies in effectively managing the pandemic. Collectively, these literature reviews significantly contribute to a nuanced and comprehensive understanding of the dynamics, spread, and strategic management of respiratory diseases, offering valuable insights for future research and public health interventions. Table 1 demonstrates some of these studies.

Figs. 1 and 2 illustrate a science mapping of various applications and research areas related to diseases from 2010 to 2023. The left picture displays distinct clusters and their interconnections, along with their sizes (number of published papers with related keywords), while the right picture showcases the distribution of publications across different years. As evident from the figures, an extensive output of more than 2.2 million research papers related to diseases is documented in the Web of Science database. Among

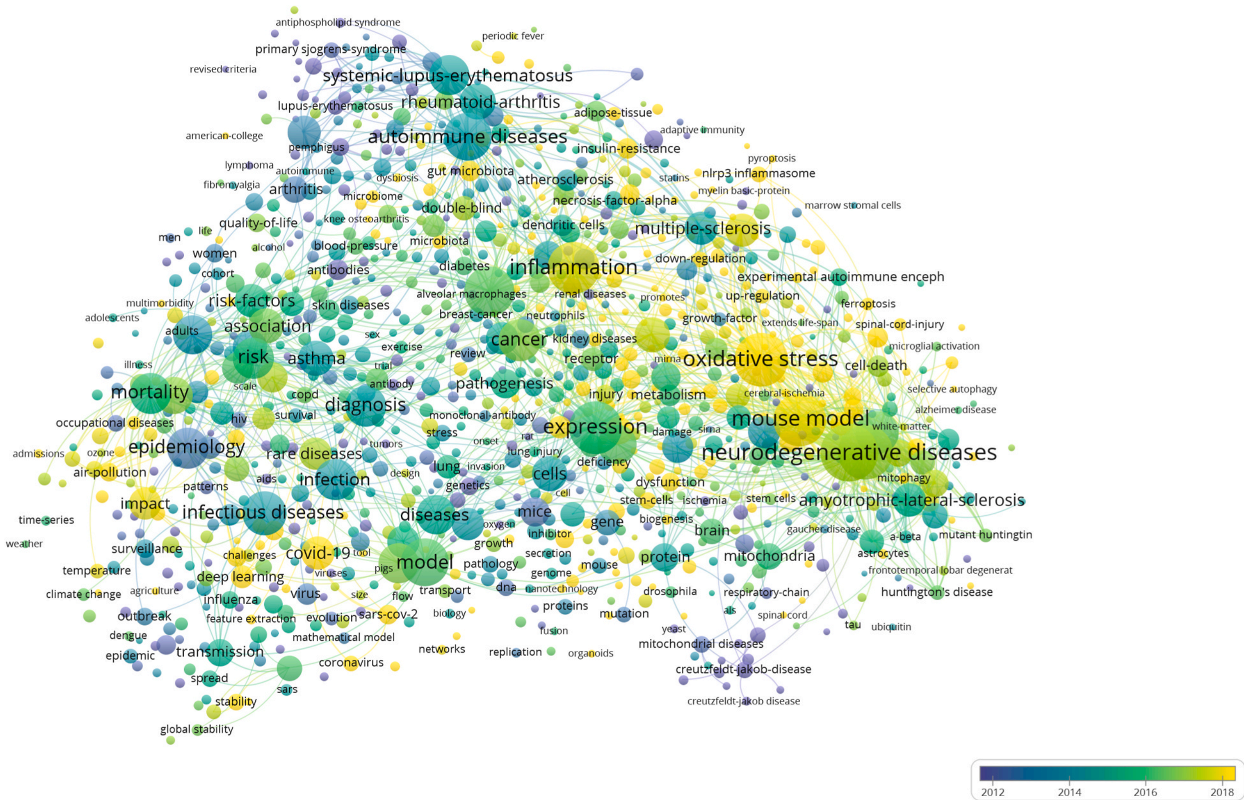

Fig. 2. A representation of map of science for date of various applications and research areas related to diseases in WoS.

these, around 50,000 papers are specifically focused on the development of systems and models for addressing these issues. Within this extensive body of literature, a smaller subset of fewer than 1000 publications has addressed respiratory virus diseases, and a mere 20 papers have explored the intricate domain of uncertainty and simulation within this particular field.

This study stands out in the expansive landscape of respiratory disease modeling by presenting an innovative SEIAR model embedded within a system dynamics analysis, addressing the intricate dynamics of societal uncertainty. Aimed at formulating optimal strategies for respiratory disease management, the research pioneers a comprehensive system-dynamics model that envisions diverse trajectories of virus diseases. Key contributions include:

- Advanced SEIAR Framework: Introducing a sophisticated SEIAR model, the research intricately integrates variables like population mobility, vaccination dynamics, and the impact of retest-positive populations on epidemic spread. This innovative framework enhances the understanding of disease dynamics within destination areas.
- Uncertainty Mitigation through EnKF and MH Algorithms: The study employs EnKF and MH algorithms to address parameter uncertainty through data assimilation. Notably, the SEIAR-EnKF framework bridges the gap between model predictions and real-world observations, refining trajectory projections with precision.
- Versatile Platform for Experimentation: The proposed framework offers versatility for both synthetic and real-world experimentation. Scenario analyses provide a comprehensive grasp of active case trends within destination areas, aiding in the anticipation and management of respiratory diseases over defined temporal intervals.

In essence, this research pioneers a meticulously designed SEIAR model integrated into subsystems, leveraging the power of system dynamics analysis. Applied to the context of Iranian COVID-19, the model proves its practicality, offering valuable insights into disease management amidst challenging circumstances. The methodologies, encompassing uncertainty accommodation and scenario-based examinations, collectively present a holistic paradigm for anticipating and addressing the complex dynamics of respiratory diseases.

Although Section 1 focuses on introduction and Section 2 provides the literature review conducted on related papers, other sections of this article are organized as follows: In Section 3, we introduce the system dynamics model proposed for respiratory virus diseases. We then apply this model to real-world data from a COVID-19 case study in Section 4, where we also showcase simulation trends. The outcomes of the proposed model are presented in Section 5, accompanied by sensitivity analyses and various scenarios for the case study. Sections 6 and 7 encompass the discussion and conclusion of this study, respectively.

3. The proposed model

We chose the SEIAR model as our mathematical foundation for capturing the evolving nature of respiratory viral diseases, using COVID-19 as a case study. By utilizing the EnKF, we seamlessly integrated data on daily confirmed cases. The MH sampling technique was employed for accurately estimating model parameters. Further elaboration on this model is presented below:

3.1. SEIAR model

In 1927, Kermack and McKendrick introduced the SIR model, a fundamental tool in epidemiology. While effective for epidemics, its relevance waned post-COVID-19 due to urban migration and vaccinations. To adapt, we extended it to SEIAR, encompassing Susceptible, Exposed, Infectious, Asymptomatic, and Removed individuals, even considering vaccinated breakthrough cases (see Fig. 3). Our dynamic model is built on SEIAR's respiratory virus insights, dissecting subsystem interplays amid uncertainty. This pioneering study blends innovation and scenario-based analysis, uniquely unraveling disease dynamics. Our equations mirror daily fluctuations of active cases, embodying our dedication to decode ever-changing disease complexities.

The following subsections are presenting the proposed model of this study in detail.

Let SI_t is susceptible individuals at the time t, EI_t is exposed individuals at the time t, SII_t is symptomatically infected individuals at the time t, AII_t is asymptomatically infected individuals at the time t, and RI_t is removed individuals (recovered or death) at the time t. Accordingly, different equations for 5 groups in the proposed uncertain SEIAR model utilized for this paper are defined as follows.

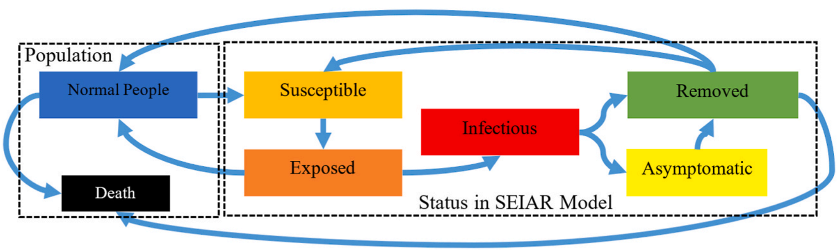

Fig. 3. A representation of SEIAR model.

3.1.1. Mathematical background

- **Susceptible individuals:** Let L_{1t} , L_{2t} are two Liu processes, μ_1, σ_1, μ_2, σ_2 are nonnegative numbers, Cr^{si}_{sii} is the contact rate between a susceptible individual and asymptomatically infected individual, Cr^{si}_{aii} is the contact rate between a susceptible individual and an asymptomatically infected individual, and Vac is vaccination rate in the susceptible individual. Then Cr^{si}_{sii} and Cr^{si}_{aii} are defined as Equations [1,2]

$$< listaend > Cr^{si}_{sii} = \mu_1 + \sigma_1 \frac{L_{1t+\Delta t} - L_{1t}}{\Delta t} \tag{1}$$

$$Cr^{si}_{aii} = \mu_2 + \sigma_2 \frac{L_{2t+\Delta t} - L_{2t}}{\Delta t} \tag{2}$$

According to equations (1) and (2), SI_t is defined as Equations [3,4]

$$SI_{t+\Delta t} - SI_t = -\left(Cr^{si}_{sii} SI_t SII_t \Delta t + Cr^{si}_{aii} SI_t AII_t \Delta t - Vac SI_t \Delta t\right) \tag{3}$$

$$\Rightarrow dSI_t = -(\mu_1 SI_t SII_t + \mu_2 SI_t AII_t - Vac SI_t)dt - \sigma_1 SI_t SII_t dL_{1t} - \sigma_2 SI_t AII_t dL_{2t} \tag{4}$$

- **Exposed individuals:** Let L_{3t} , L_{4t} are two Liu processes, μ_3, σ_3, μ_4, σ_4 are nonnegative numbers, R^{ei}_{sii} is the rate that exposed individuals become symptomatically infected individuals, and R^{ei}_{aii} is the rate that exposed individuals become asymptomatically infected individuals. Then R^{ei}_{sii} and R^{ei}_{aii} are defined as Equations [5,6]

$$< listaend > R^{ei}_{sii} = \mu_3 + \sigma_3 \frac{L_{3t+\Delta t} - L_{3t}}{\Delta t} \tag{5}$$

$$R^{ei}_{aii} = \mu_3 + \sigma_3 \frac{L_{3t+\Delta t} - L_{3t}}{\Delta t} \tag{6}$$

According to equations (5) and (6), EI_t is defined as Equations [7,8]

$$EI_{t+\Delta t} - EI_t = (SI_t - SI_{t+\Delta t}) - \left(R^{ei}_{sii} + R^{ei}_{aii}\right) EI_t \Delta t \tag{7}$$

$$\Rightarrow dEI_t = (\mu_1 SI_t SII_t + \mu_2 SI_t AII_t - \mu_3 EI_t - \mu_4 EI_t)dt + \sigma_1 SI_t SII_t dL_{1t} + \sigma_2 SI_t AII_t dL_{2t} - \sigma_3 EI_t dL_{3t} - \sigma_4 EI_t dL_{4t} \tag{8}$$

- **Symptomatically infected individuals:** Let L_{5t}, L_{6t} are two Liu process, μ_5, σ_5, μ_6, σ_6 are nonnegative numbers, Rr^{sii}_{rod} is the removed (death) rate of symptomatically infected individuals, and Rr^{sii}_{ror} is the removed (recovered) rate of symptomatically infected individuals. Then Rr^{sii}_{rod} and Rr^{sii}_{ror} are defined as Equations [9,10]

$$< listaend > Rr^{sii}_{rod} = \mu_5 + \sigma_5 \frac{L_{5t+\Delta t} - L_{5t}}{\Delta t} \tag{9}$$

$$Rr^{sii}_{ror} = \mu_6 + \sigma_6 \frac{L_{6t+\Delta t} - L_{6t}}{\Delta t} \tag{10}$$

According to equations (5), (9) and (10), SII_t is defined as Equations [11,12]

$$SII_{t+\Delta t} - SII_t = R^{ei}_{sii} EI_t \Delta t - \left(Rr^{sii}_{rod} SII_t \Delta t + Rr^{sii}_{ror} SII_t \Delta t\right) \tag{11}$$

$$\Rightarrow dSII_t = (\mu_3 EI_t - (\mu_5 SII_t + \mu_6 SII_t))dt + \sigma_3 EI_t dL_{3t} - (\sigma_5 SII_t dL_{5t} + \sigma_6 SII_t dL_{6t}) \tag{12}$$

- **Asymptomatically infected individuals:** Let L_{7t}, L_{8t} are two Liu process, μ_7, σ_7, μ_8, σ_8 are nonnegative numbers, Rr^{aii}_{rod} is the removed (death) rate of asymptomatically infected individuals, and Rr^{aii}_{ror} is the removed (recovered) rate of asymptomatically infected individuals. Then Rr^{aii}_{rod} and Rr^{aii}_{ror} are defined as Equations [13,14]

$$< listaend > Rr^{aii}_{rod} = \mu_7 + \sigma_7 \frac{L_{7t+\Delta t} - L_{7t}}{\Delta t} \tag{13}$$

$$Rr^{aii}_{ror} = \mu_8 + \sigma_8 \frac{L_{8t+\Delta t} - L_{8t}}{\Delta t} \tag{14}$$

According to equations (6), (13) and (14), AII_t is defined as Equations [15,16]

$$AII_{t+\Delta t} - AII_t = R^{ei}_{aii} EI_t \Delta t - \left(Rr^{aii}_{rod} AII_t \Delta t + Rr^{aii}_{ror} AII_t \Delta t\right) \tag{15}$$

$$\Rightarrow dAII_t = (\mu_4 EI_t - (\mu_7 AII_t + \mu_8 AII_t))dt + \sigma_4 EI_t dL_{4t} - (\sigma_7 AII_t dL_{7t} + \sigma_8 AII_t dL_{8t}) \tag{16}$$

- **Removed individuals:** According to equations (9), (10), (13) and (14), RI_t is defined as Equations [17,18]

$$< listaend > RI_{t+\Delta t} - RI_t = Rr^{sii}_{rod} SII_t \Delta t + Rr^{sii}_{ror} SII_t \Delta t + Rr^{aii}_{rod} AII_t \Delta t + Rr^{aii}_{ror} AII_t \Delta t \tag{17}$$

$$\Rightarrow dRI_t = (\mu_5 SII_t + \mu_6 SII_t + \mu_7 AII_t + \mu_8 AII_t)dt + \sigma_5 SII_t dL_{5t} + \sigma_6 SII_t dL_{6t} + \sigma_7 AII_t dL_{7t} + \sigma_8 AII_t dL_{8t} \tag{18}$$

According to equations ((4), (8), (12), (16) and (18), the uncertain SEIAR model is proposed to model an epidemic disease in a social system based on uncertain behavior of people, where SI_t: susceptible individuals, EI_t: exposed individuals, SII_t: symptomatically infected individuals, AII_t: symptomatically infected individuals, RI_t: removed individuals, L_{it}: Liu processes, μ_i and σ_i for $i = 1, \ldots, 8$ are nonnegative numbers. It is noteworthy that the uncertain SEIR model is degenerates if $AII_t = \mu_4 = \sigma_4 = 0$. In addition, the uncertain SIR model is an uncertain SEIR if $EI_t = \mu_2 = \sigma_2 = 0$. Therefore, the proposed uncertain SEIAR model in this paper can degenerate uncertain SEIR and uncertain SIR models, as well. Real data about susceptible individuals, exposed individuals, symptomatically infected individuals, asymptomatically infected individuals, and removed individuals for previous days could be utilized in these equations to find appropriate variables for this model. SI_0 is equal to all populations of each country and t is the number of days with the determined number of infectious diseases patients. Besides, $\frac{L_{jt_{i+1}} - L_{jt_i}}{t_{i+1} - t_i}$ is a standard normal uncertain variable N(0,1) based on the definition of Liu process. Therefore, all μ_i and σ_i are predicted based on the mentioned information.

3.1.2. The main subsystem of disease spread

The literature indicates universal susceptibility to respiratory viruses, with birth and mortality rates based on WHO reports. The infected are categorized as asymptomatic, symptomatic, and then divided into recovery or fatality groups. After about 14 days, the recovered can still be transmitted to susceptible people. Individual traits like gender and age, along with uncertain community behaviors, shape disease estimates. Combined with the SEIAR model, a dynamic system model is formed, factoring in temperature's impact on transmission. Explore Fig. 4 and Table 2 for deeper insights into the spread subsystem of the model.

Various factors are established according to the starting model and existing data. Certain factors are categorized as "level" variables, as they derive from the integration of other variables known as "rate" variables. These connections between level and rate variables are indicated by black arrows. Additional relationships are depicted by blue arrows. A subset of variables remains constant throughout and is defined as such. Auxiliary variables are shaped by predefined functional forms and functions based on other variables. Shadow variables, denoted by pale shading and parentheses, operate independently. When a pathway exists between variables along the arrow direction, a loop forms within the model.

The current information from the proposed model falls short in demonstrating how various policies affect disease control. To address this, we delve into distinct sectors like healthcare, transportation, food, drug distribution networks, contacts, and their influences on the uncertain SEIAR model's parameters. Herein, we present a breakdown of the subsystems:

3.1.3. Healthcare subsystem

The healthcare system plays a vital role in this model, given the substantial impact of hospitals and healthcare centers on disease control. Initial variables are derived from literature, while additional ones stem from available data. These variables' parameters can be fine-tuned using Ministry of Health reports from each country. By establishing intricate relationships within this subsystem, it seamlessly integrates with the spread subsystem of the proposed dynamic model. This component assesses the capacity of hospitals and healthcare centers to accommodate patients, adjusting allocated beds based on patient numbers and system capacity. Vaccination serves as a critical factor for susceptible individuals. Furthermore, the healthcare system's influence on recovery and mortality rates factors in patient accessibility to different centers. For a deeper dive, refer to Fig. 5 and Table 3.

3.1.4. Transportation subsystem

An essential component is the transportation subsystem, a vital aspect of daily life categorized into public and private modes. Initial

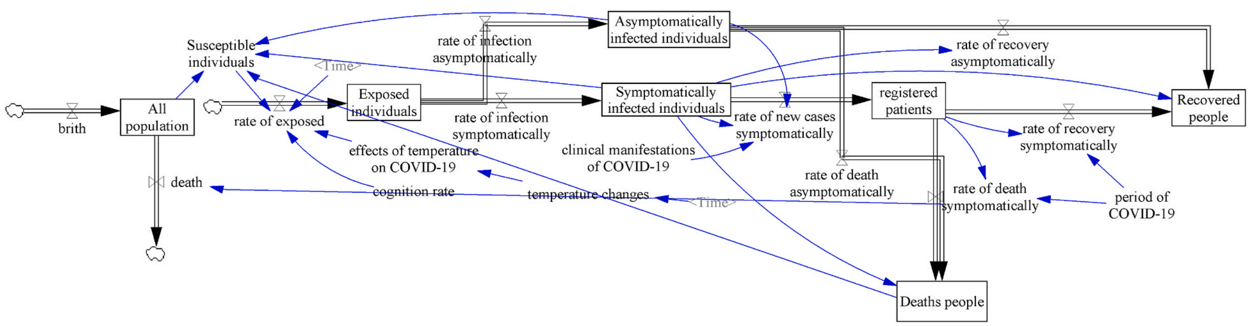

Fig. 4. A representation of the spread subsystem of the proposed model.

Table 2
Definition of the spread subsystem of the proposed model.

Variable name	Definition	Type	Relationship
Birth	The average number of people born per month	Auxiliary	predefined functional forms
Death	The average number of deaths per month	Auxiliary	predefined functional forms
All population	The population of country	Level	function
Susceptible individuals	The susceptible population is 95 % of country people	Auxiliary	function
rate of exposed	Exposed rate for infectious	Auxiliary	functional forms
Time	The time variable used in the model	Constant	constant
Exposed individuals	The exposed people	Level	function
effects of temperature	The effect of temperature on virus function	Auxiliary	predefined functional forms
temperature changes	Average temperature changes during a year in country	Auxiliary	predefined functional forms
cognition rate	Cognition rate of virus	Constant	predefined functional forms
rate of infection symptomatically	The rate of infected people with symptoms	Auxiliary	functional forms
rate of infection asymptomatically	The rate of infected people without symptoms	Auxiliary	functional forms
Symptomatically infected individuals	The number of infected people with symptoms	Level	function
Asymptomatically infected individuals	The number of infected people without symptoms	Level	function
rate of new cases symptomatically	Rate of patient addition to confirmed patients with symptoms	Auxiliary	functional forms
clinical manifestations of disease	The average time between infection and the first sign of symptoms	Constant	constant
registered patients	Number of confirmed patients	Level	function
rate of recovery symptomatically	Recovery rate for symptomatic infected people	Auxiliary	functional forms
rate of recovery asymptomatically	Recovery rate for asymptomatic infected people	Auxiliary	functional forms
rate of death symptomatically	Mortality rate for symptomatic infected people	Auxiliary	functional forms
rate of death asymptomatically	Mortality rate for asymptomatic infected people	Auxiliary	functional forms
period of infection	The average time of infection	Constant	predefined functional forms
Recovered people	The number of people who recovered	Level	function
Deaths people	The number of people who died	Level	function

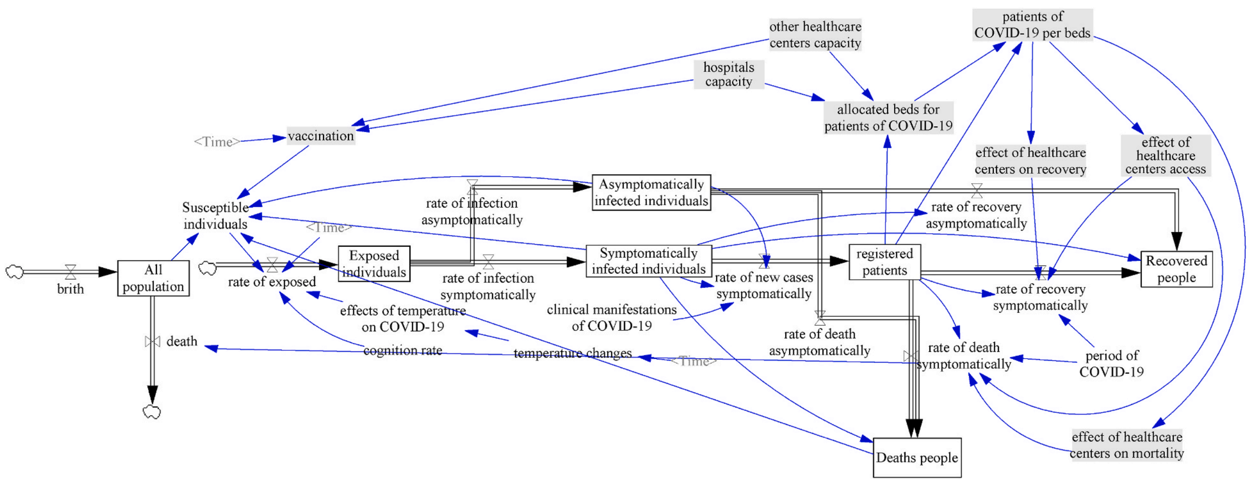

Fig. 5. The spread subsystem of the proposed model and healthcare subsystem.

Table 3
Definition of the healthcare subsystem model.

Variable name	Definition	Type	Relationship
hospitals capacity	The capacity of the number of beds in the hospitals	Constant	constant
other healthcare centers capacity	The capacity of the number of beds in other healthcare centers	Constant	constant
allocated beds for patients	Number of allocated beds to the patients	Auxiliary	functional forms
patients per beds	The ratio of the number of patients to the number of allocated beds	Auxiliary	function
effect of healthcare centers on recovery	The effect of hospital services on patient recovery	Auxiliary	functional forms
effect of healthcare centers access	The effect of hospitals access on their services	Auxiliary	functional forms
effect of healthcare centers on mortality	The effect of hospital services on patient mortality	Auxiliary	functional forms
Vaccination	The effect of vaccination on susceptible individuals	Auxiliary	functional forms

parameters are derived from literature, while additional ones stem from available data. Capacity, sourced from the Ministry of Roads and Transportation reports, shapes both parts. Public transportation significantly influences social interactions, with infection rates escalating. Raising infection awareness encourages private vehicle use. This dynamic element is incorporated in our system model

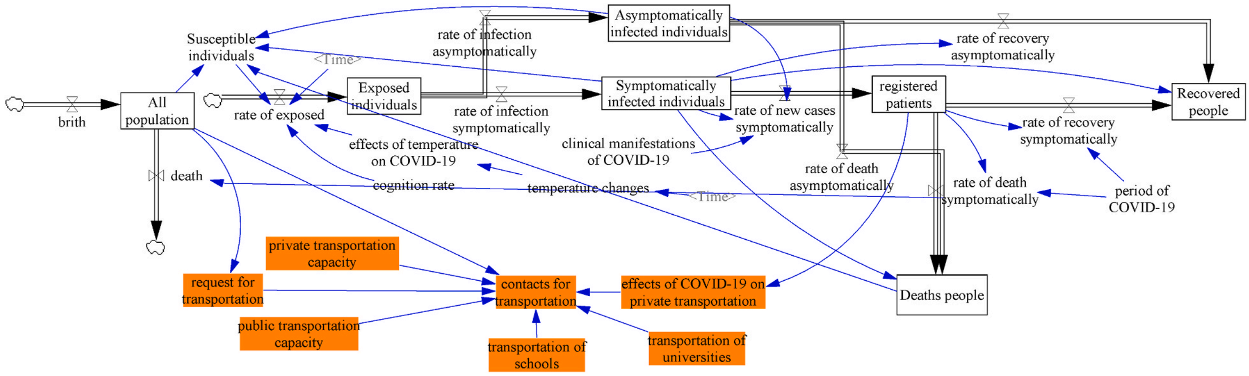

Fig. 6. The spread subsystem of the proposed model and transportation subsystem.

(Fig. 6), with further details in Table 4. The model considers various modes for work, shopping, leisure, etc., accounting for public and private contexts. Notably, shifts in these modes during and post-lockdown couldn't be appraised due to data constraints, except for educational institutions, included for data clarity.

3.1.5. *Food and drug distribution subsystem*

Food and drug distribution networks play a crucial role in population density. While some variables are derived from literature, others stem from available data. These networks must meet the people's needs; a surge in demand post-infection news drastically affects infection rates. As per the health ministries, changing the capacities of these centers takes time. Managing this requires tracking demand shifts. Check out Fig. 7 for an overview of the spread subsystem in our dynamic model and Table 5 for additional insights.

3.1.6. *Contact subsystem*

The healthcare subsystem significantly impacts the proposed model's spread subsystem, both directly and indirectly. While the transportation and food-drug network subsystems exert indirect influence on the spread subsystem, they play a crucial role in shaping the frequency of interactions among individuals. This underscores the importance of including the contacts subsystem within our proposed model. For more insights on this subsystem, refer to Fig. 8 and Table 6.

The paper introduces a system dynamics model based on infectious disease dynamics and its interconnected subsystems: healthcare, transportation, food and drug networks, and contacts. Each subsystem is demarcated with distinct colors, defining their boundaries. Fig. 9 vividly showcases the dynamic model, offering a visual journey through these interconnected subsystems.

Numerous subsystems contribute to the study of human societies, introducing complexities when incorporated into models. To guide dynamic system models, it's crucial to identify both direct and indirect subsystems. In this study, we employ an uncertain SEIAR model to simulate respiratory disease outbreaks, encompassing healthcare, transportation, food-drug distribution, and contacts as key subsystems with direct impacts. While other influential subsystems exist, their effects are indirectly addressed within this framework. For instance, the education subsystem indirectly influences transportation and contact dynamics. Additionally, the work environment, a potent subsystem, directly impacts contact and transportation patterns. Thus, our model focuses on direct impact subsystems, while acknowledging the nuanced influence of other elements.

3.1.6.1. Ensemble Kalman Filter. The Ensemble Kalman Filter (EnKF) is a powerful algorithm employed in the context of epidemic modeling, acting as a maestro in refining predictions and mitigating bias within nonlinear models such as SEIAR. In essence, the EnKF can be visualized as a conductor orchestrating a symphony of accuracy, dynamically integrating daily observations to enhance the precision of vital state variables.

EnKF's strength lies in its ability to assimilate real-world data into models seamlessly, ensuring that predictions align closely with observed outcomes. This iterative dance of forecasting and analysis is akin to a ballet, where each observation gracefully contributes to refining the model's trajectory.

Table 4
Definition of the transportation subsystem model.

Variable name	Definition	Type	Relationship
effects of infection on private transportation	The effect of infection on the use of private vehicles	Auxiliary	functional forms
contacts for transportation	The average number of visits per transport	Auxiliary	predefined functional forms
private transportation capacity	The average capacity of personal transportation	Auxiliary	constant
public transportation capacity	The average capacity of public transportation	Auxiliary	constant
request for transportation	Average of requests for transportation	Auxiliary	function
transportation for schools	Average of requests for schools' transportation	Auxiliary	functional forms
transportation for universities	Average of requests for universities' transportation	Auxiliary	functional forms

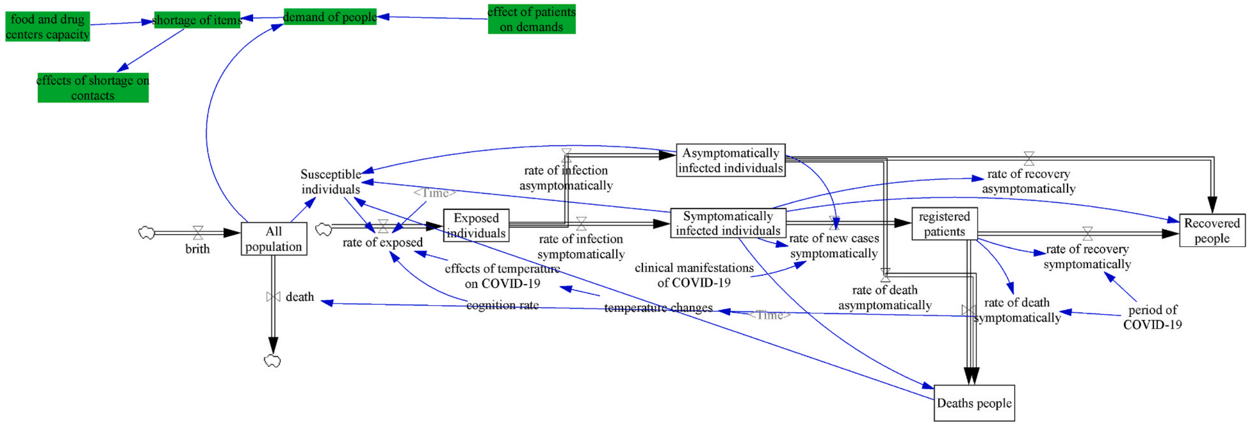

Fig. 7. The spread subsystem of the proposed model with food and drug subsystem.

Table 5
Definition of food and drug networks subsystem model.

Variable name	Definition	Type	Relationship
effect of patients on demands	The effect of the news about infection on the demand for medicinal substances and foodstuffs	Auxiliary	functional forms
demand of people	The average demand of the people	Auxiliary	function
shortage of items	The average shortage of various items	Auxiliary	function
food and drug centers capacity	The average distribution capacity of pharmaceutical and food centers	Constant	predefined functional forms
effects of shortage on contacts	The effects of average shortages of different items on the number of contacts	Auxiliary	functional forms

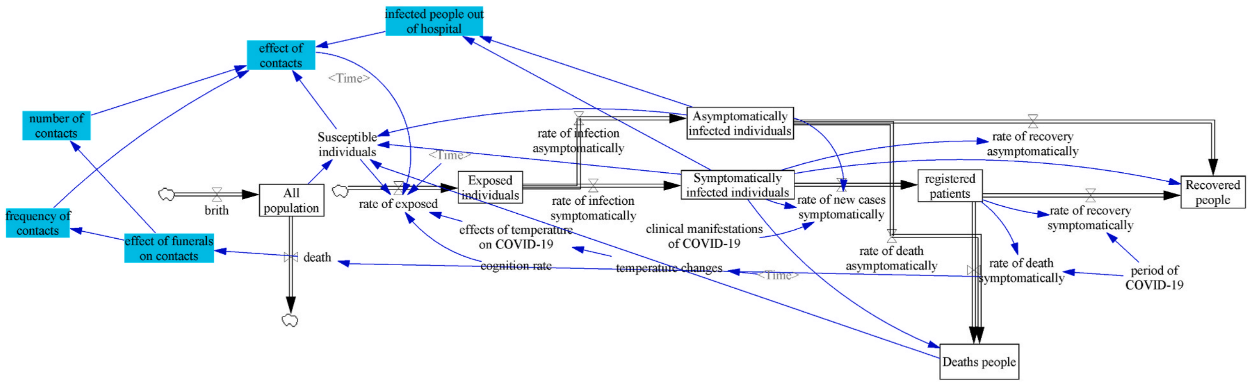

Fig. 8. The spread subsystem of the proposed model with contacts subsystem.

Table 6
Definition of contacts subsystem model.

Variable name	Definition	Type	Relationship
infected people out of hospital	The average number of infected people outside of the hospitals	Auxiliary	function
effect of contacts	The effect of contacts on the rate of infection	Auxiliary	functional forms
effect of funerals on contacts	The effect of deaths on contacts	Auxiliary	functional forms
frequency of contacts	The average frequency of contacts	Auxiliary	functional forms
number of contacts	The average number of contacts	Auxiliary	functional forms

A key feature of EnKF is its ensemble approach, which uses multiple simulations to represent the uncertainty associated with model parameters. This ensemble strategy contributes to operational efficiency, and the statistical techniques employed by EnKF effectively eliminate the biases that may arise in predictions. The algorithm's proficiency in harmonizing epidemic history with real-time

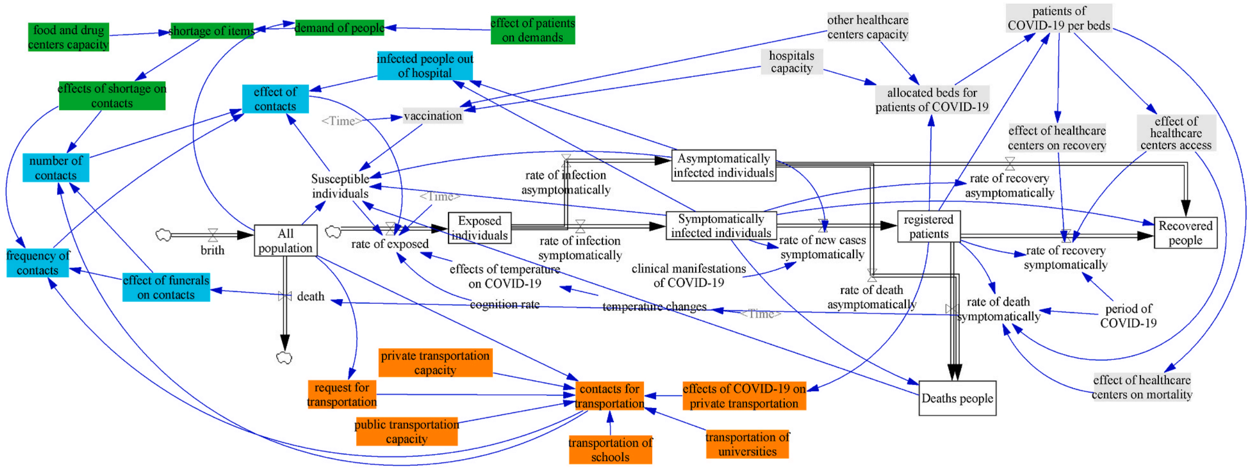

Fig. 9. A representation of the proposed system dynamics model.

observations makes it a shining star in the realm of data assimilation, providing a robust tool for enhancing the accuracy of infectious disease modeling. Behold the unfolding of EnKF's steps:

Step 1. A Grand Beginning

1.1. We summon a cast of ensemble members (N) to represent the tapestry of initial uncertainty.

1.2. Each ensemble member strides onto the stage, a unique portrayal of the initial state, painted with random splashes of noise or drawn from a distribution of uncertainty.

Step 2. A Vision of Tomorrow (Model Prediction)

2.1. Every member embarks on a journey through time, dancing to the rhythm of the dynamic model.

2.2. Echoes of uncertainty are woven into their choreography, as model noise and perturbations infuse diversity into the ensemble's graceful trajectories.

Step 3. Harmonizing Reality (Observation Preprocessing)

3.1. Real-world observations join the performance, each note resonating with measurements and their own unique uncertainties.

3.2. Anomalies ripple through the ensemble, the difference between observations and the dancers' predictions, casting a spell of intrigue.

Step 4. The Transformation (Analysis Update - Ensemble Perturbation)

4.1. Ensemble mean takes the spotlight alongside the deviations from the mean, the very heartbeat of state and observation anomalies.

4.2. A ″3-2″ metamorphosis begins: the Kalman gain appears, connecting observation anomalies with state perturbations.

4.3. The dance evolves into an analysis, a fusion of Kalman's grace, observation anomalies' mystique, and state perturbations' allure.

Step 5. Reshaping Reality (Analysis Update - State Reconstruction)

5.1. The analysis ensemble takes center stage, the sum of updated perturbations and the mean's poise.

5.2. The analysis state steps into the limelight, the culmination of ensemble synergy, a snapshot of refined reality.

Step 6. The Eternal Cycle (Data Assimilation)

6.1. The dance continues, each step a mirror of the past ones, a cadence of Steps 2 through 5.

6.2. The analysis state leads the ensemble, a torchbearer of insight, igniting the next scene.

6.3. As new observations join the ensemble, the dance transforms, a perpetual evolution of ensemble and analysis.

Ensemble Kalman Filter unfolds as an iterative masterpiece, reprising Steps 2 to 6 with each assimilation moment. It's a harmonious duet between model predictions and real-world observations, a ballet of uncertainty where ensemble trajectories waltz to reveal the truth behind the scenes. EnKF's harmony surfaces as a beacon of precision for epidemic prevention strategies. Coupled with daily observations, it's the key to tuning simulation accuracy and bridging the gap between foresight and actuality. This journey is an ongoing symphony of forecasting and analysis, refining state variable estimates through the chorus of observations. Forecasting is the echo of history and the bridge to the future. The fusion of predictions and observations births optimal enlightenment. In the realm of analysis, intricate mathematical pas de deux elevate these estimations, a testament to unrivaled precision.

3.2. Metropolis-Hastings algorithm

The Metropolis-Hastings (MH) algorithm is a powerful tool for tackling the challenges of parameter uncertainty, particularly in the complex landscape of the SEIAR model. Unlike some other algorithms, the MH algorithm excels in its simplicity, allowing it to navigate through iterations and sample distributions without an intricate understanding of their shapes. This quality makes it especially valuable when dealing with the multifaceted dynamics of estimating model parameters in the SEIAR framework.

The algorithm unfolds in a series of distinct steps, each contributing to the precision of parameter estimation. It begins with the identification of choice points, strategically generating candidate values. These candidates are then subjected to an anticipation of potential outcomes and a quantification of their likelihoods, given the available data. The algorithm then calculates the odds of accepting these candidates, a crucial step in determining their contribution to the overall parameter space. As the iterations progress, the algorithm steadily converges towards optimal model parameters, ensuring a thorough exploration of the parameter space.

While the MH algorithm may not be the fastest at achieving convergence, its deliberate and methodical approach conceals a rich narrative. Each iteration contributes to the algorithm's understanding of the parameter landscape, effectively balancing the acceptance probabilities of the generated candidates. One of the algorithm's remarkable strengths lies in its ability to handle intricate distributions with ease. This liberates practitioners from the burden of needing a deep understanding of the underlying distribution shapes, simplifying the parameter estimation process, especially in the dynamic and uncertain context of the SEIAR model. In the context of SEIAR model parameter estimation, the MH algorithm emerges as a beacon of reliability amidst uncertainty. Its streamlined approach illuminates the path to obtaining dependable model parameters, offering a valuable contribution to the broader field of infectious disease modeling and enhancing our ability to comprehend and manage public health crises. Guided by its principles, the MH algorithm plays a crucial role in navigating the complexities of parameter uncertainty, facilitating robust and informed decision-making in public health contexts.

Let's venture into the world of the MH algorithm, an ingenious MCMC approach designed to unravel the enigma of parameter uncertainty:

- Initialization: Begin with initial values denoted as θ for the parameters to be estimated. These initial values can be chosen randomly or based on prior knowledge.
- Creating Candidates: Craft a candidate parameter set, θ_{new}, using a proposal distribution $q(\theta_{new} |\theta)$. This distribution dictates how you transition from the current parameter values to new ones in each iteration.
- Likelihood Evaluation: Calculate the likelihood of your data given the candidate parameter set, denoted as $L(\theta_{new})$. This reflects how well the model with the candidate parameters aligns with the observed data.
- Acceptance Probability Computation: Compute the acceptance probability, α, which determines whether to embrace or reject the candidate parameters. It's calculated as:

$$\alpha = \min(1, L(\theta_{new}) / L(\theta_{current}) *q(\theta_{current} \mid \theta_{new}) / q(\theta_{new} \mid \theta_{current}))$$

Here, $\theta_{current}$ represents the current parameter values.

- Acceptance or Rejection: Roll a dice with values between 0 and 1. If the rolled value is less than or equal to the acceptance probability α, embrace the candidate parameters (set $\theta = \theta_{new}$). Otherwise, let them go (keep θ unchanged).
- Iteration: Move on to the next iteration. If you accepted the candidate parameters, they become the new current parameters. If not, the current parameters remain intact.
- Repeat: Recur through steps 2 to 6 for a predefined number of iterations or until convergence criteria are satisfied.

Operating as a Markov chain, the MH algorithm's each step relies solely on the present state and the proposed one. Across iterations, it charts a course through the parameter space, striving to capture samples from the genuine underlying parameter distribution. While the algorithm may take its time to converge, it shines when faced with complex distributions or situations where direct sampling proves challenging.

Keep in mind that the choice of the proposal distribution $q(\theta_{new} |\theta)$ is pivotal. If too narrow, the algorithm could wander slowly through parameter space. If too broad, acceptance rates might dwindle, causing inefficient sampling. Tailoring the proposal distribution and iteration count becomes key for effective parameter estimation. The voyage set in motion by the MH algorithm is not a sprint to the finish line. Its measured pace echoes within each iteration, where candidate selection and acceptance probability calculations paint a mesmerizing picture. What truly stands out is the algorithm's ability to conquer distribution complexities, making it a champion at deciphering intricate patterns. While the MH algorithm takes its time to converge, its partnership with the agile SEIAR model ensures a harmonious rhythm, crafting an enthralling narrative of parameter estimation.

In a domain ruled by uncertainty, the MH algorithm stands tall as a sentinel of hope. Its simplicity gracefully dances alongside the shadows of alternative methodologies, discarding the need for intricate equations to embrace the core of distribution forms. Hence, complexity bows before its might, revealing a path paved with reliable parameters for the radiant realm of SEIAR models.

3.2.1. Structure of the proposed model

In this study, we enhance the SEIAR model by integrating observed active cases to iteratively estimate both states and parameters. We conducted an extensive analysis spanning over 1300 days, exploring various epidemic control strategies through a blend of synthetic and real-world experiments. By examining diverse trends in active cases across different parameter setups, we shed light on experimental insights. These findings are contrasted with RMAEs between predictions, analyses, and observations while addressing parameter uncertainty using the MH sampling method. The proposed model's workflow is depicted in Fig. 8, capturing its structure and real-world applicability. Fig. 10 showcases scene selection, encompassing synthetic and Iranian real-world routes, whereas MH and EnKF illustrate the parameter estimation process and data assimilation, delineating the distinct paths for synthetic and real-world experiments. The assimilation process, pivotal for updating predictions, varies based on preset parameters or the parameter estimation journey. The comprehensive SEIAR-EnKF framework in this study visually portrays the divergent routes, offering a deeper grasp of both synthetic and real-world scenarios.

Regarding the mentioned description, the proposed model is a novel integration of the SEIAR framework within a system dynamics analysis, introducing uncertainty through Liu processes and advanced algorithms like Ensemble Kalman Filter and Metropolis-Hastings. This innovative approach aims to enhance community health management, specifically targeting respiratory virus diseases such as COVID-19.

The model's key assumptions are supported by biological evidence. For instance, the incorporation of uncertain parameters reflects the inherent unpredictability in the dynamics of infectious diseases, mirroring the variability observed in real-world scenarios. The consideration of population mobility, vaccination dynamics, and retest-positive populations in the SEIAR framework aligns with the complex and multifactorial nature of virus transmission.

Furthermore, the model acknowledges the varying mortality rates observed across scenarios in Iran during real COVID-19 outbreaks. This aligns with the biological reality that the severity and impact of respiratory viruses can differ significantly based on contextual factors, including healthcare infrastructure, demographics, and public health interventions.

In terms of its novelty, the model represents a significant advancement in infectious disease modeling. While it builds upon the SEIAR structure, the integration of uncertain parameters, Liu processes, and advanced algorithms distinguishes it as a unique contribution to the field. This novel approach allows for a more realistic representation of the inherent uncertainties in disease dynamics and improves the model's predictive accuracy. In summary, the proposed model introduces a fresh perspective to infectious disease modeling, supported by biological rationale and novel elements. It combines well-established frameworks with innovative features to provide a comprehensive tool for community health management in the context of respiratory virus diseases.

4. Case study: COVID-19 in Iran

Respiratory viruses, widespread contributors to global human disease, have been comprehensively studied, including those introduced in Section 1. However, the spotlight today is on COVID-19, the renowned viral illness. To unravel its impact, we employ the innovative SEIAR uncertain model with distinct subsystems, focusing on COVID-19 prevalence in Iran, ranked 19th by WHO in August 2023. The SEIAR model parameters are meticulously tuned to align with historical data from http://www.worldometers.info/for Iran. Additional subsystem parameters are seamlessly integrated, upholding result consistency and logical coherence. The stepwise incorporation of each subsystem undergoes rigorous verification, ensuring result accuracy and trend fidelity.

This selection ensures relevance and real-world applicability, as Iran faces unique challenges, including international constraints.

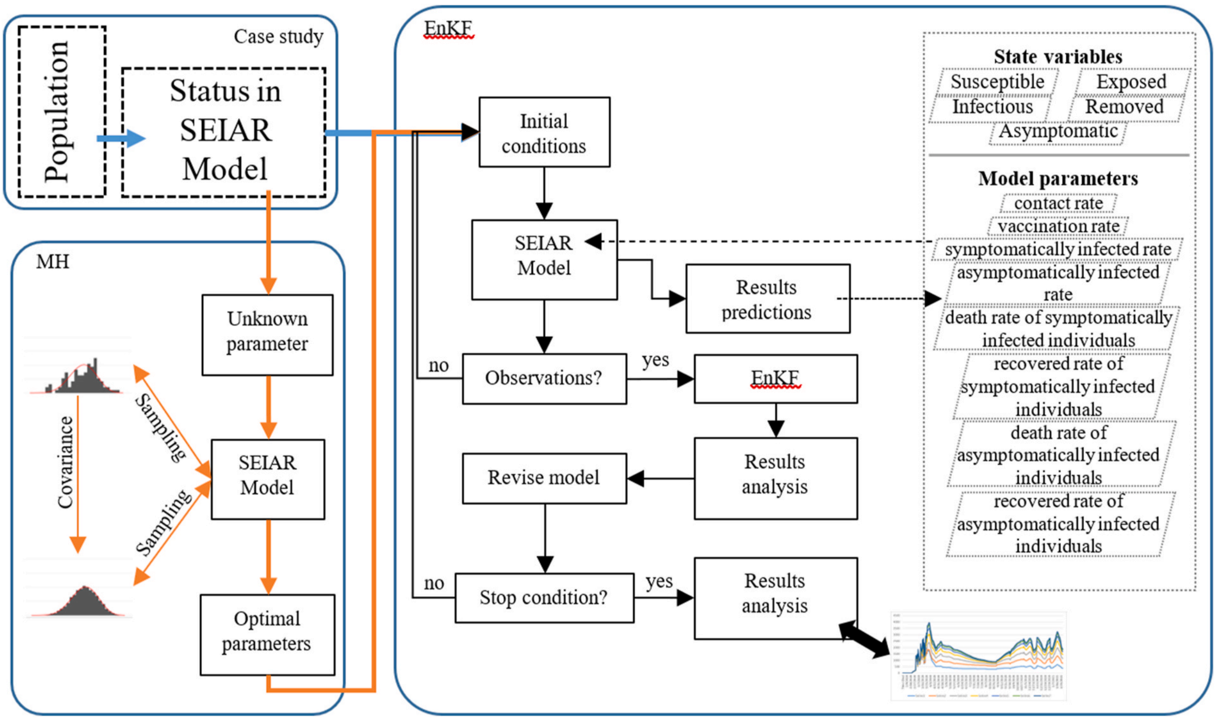

Fig. 10. Representation for structure of the proposed model.

The SEIAR uncertain model, tailored to Iranian data from reliable sources, enables a comprehensive analysis of COVID-19 dynamics. The findings from Iran hold applicability to diverse contexts for several reasons. First, the systemic model framework, including the SEIAR model and distinct subsystems, offers flexibility for adaptation to different geographical and socio-economic settings. Second, the scenario-based analyses conducted provide a versatile approach that can be replicated in other regions. Third, the study's insights contribute to global health management by offering lessons and strategies applicable to countries dealing with similar respiratory disease outbreaks.

4.1. Simulation of the trends

The paper introduces a comprehensive model comprising interconnected subsystems addressing disease spread, healthcare, transportation, and food/drug supply, alongside contact patterns. Employing Python 3.11.5, Anaconda3 2023.03, and Vensim 7.3.5 on a personal computer with Intel (R) Core (TM) i5-11400H CPU @ 2.70 GHz and 16.00 GB RAM, the model is simulated for analysis. After fine-tuning with available data, the model predicts various future trends. Historical data spanning 1302 days (Feb 1, 2020 to Aug 25, 2023) is gathered from worldometers site. Simulation outcomes align well with historical trends (Fig. 11). Rigorous system dynamics tests including boundary, structure, consistency, extreme conditions, and reproduction assessments confirm the model's effectiveness, notably demonstrated by the NRMSD results. NRMSD is a normalized measure of the differences between values predicted by a model and the values observed. According to literature review, NRMSD is equal to $\frac{RMSD}{x_{max}-x_{min}}$ where $RMSD = \sqrt{\frac{\sum_{i=1}^{n}(x_i-\widehat{x_i})^2}{n}}$ and $\widehat{x_i}$ is estimated parameter of x_i as one of n observed parameters. NRMSD values for daily new cases, deaths, and recoveries stand at 0.2 %, 1.2 %, and 0.6 % respectively, indicating minor average errors of under 108 cases, 8 deaths, and 224 recoveries per day. Notably, the average daily figures are 5848 new cases, 112 deaths, and 5664 recoveries. This robustly validates the model's accuracy.

A refined model leveraging historical data anticipates forthcoming trends guided by the subsequent premises:

- Projections encompass a 1302-day period (Feb 1, 2020 to Aug 25, 2023) for Iran, envisioning the aftermath of the novel respiratory virus, COVID-19 in different scenarios.
- The model deliberately omits conventional inter-country travel scenarios, attributing this to global quarantine measures and novel regulations;

5. Results

5.1. Sensitivity analysis

The proposed dynamic system model involves several parameters essential for predicting the count of infections, recoveries, and fatalities. While some variables are predetermined using country-specific data (e.g., population), the Design of Experiments plays a pivotal role in estimating unknown parameters based on a nation's disease reports. In this case study, all unknown parameters were meticulously calibrated using proposed model. This ensured that the final model's outcomes aligned seamlessly with recorded data. Now, let's delve into the intriguing aspects of the model's key parameters:

- Impact of Daily New Cases on Demand (P1): This parameter underscores how reports of new infections shape societal demand by influencing public perceptions.
- Shortages' Influence on Contacts (P2): Escalating demand and resulting shortages trigger more interactions as individuals seek out scarce commodities and engage with sellers.
- Funeral-Driven Contacts (P3): A surge in deaths amplifies visits among people, intensifying the frequency of social interactions.
- Private vs. Public Transport (P4): Awareness campaigns about the disease steer individuals toward private transport for safety, impacting infection rates and transportation preferences.

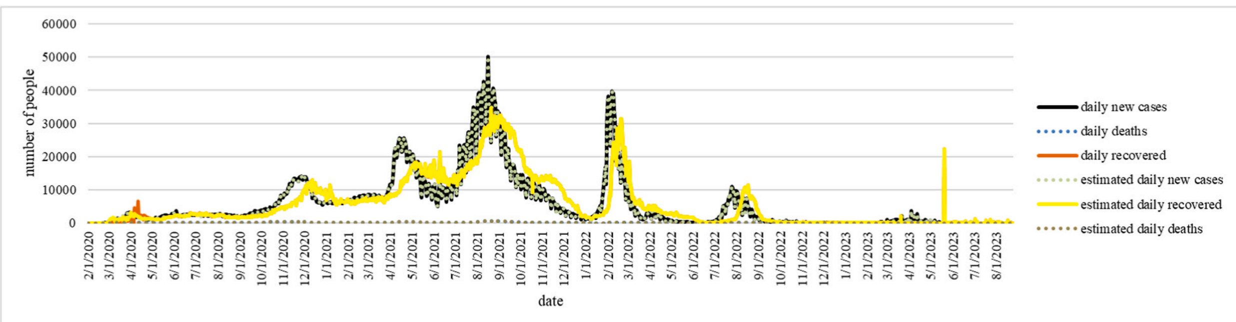

Fig. 11. Simulated number of daily new cases, daily deaths, and daily recovered versus real data.

Table 7
Effects of every coefficient on every selected parameter in the proposed model.

Coefficient	parameters	summation of daily new cases	summation of daily recovered	summation daily deaths	summation of daily new cases	summation of daily recovered	summation daily deaths	parameters	coefficient
0.1	P1	0.773	0.772	0.773	1.322	1.322	1.322	P1	10
	P2	0.438	0.432	0.438	1.285	1.285	1.285	P2	
	P3	0.341	0.334	0.341	1.263	1.263	1.263	P3	
	P4	7.774	7.831	7.773	0.701	0.701	0.702	P4	
	P5	0.226	0.226	0.225	2.543	2.448	2.539	P5	
	P6	1.484	1.576	1.415	0.801	0.738	0.738	P6	
	P7	1.017	1.089	1.109	0.786	0.723	0.715	P7	

- Contact Dynamics (P5): Adhering to health guidelines, including mask usage and physical distancing, curbs infection probabilities by modifying interpersonal contacts.
- Healthcare Centers' Role in Recovery (P6): Bolstering medical facilities enhances patient recovery rates, accentuating the healthcare system's pivotal role.
- Healthcare Centers' Impact on Mortality (P7): Similarly, healthcare centers play a crucial role in mortality rates, shedding light on their indispensable contribution.

These unknown parameters $P_i \quad i \in (1, \ldots, 7)$ are meticulously estimated to harmonize the final model with observed data. Each parameter is assigned a coefficient of 1 in normal scenarios, wielding distinct effects on the model (The coefficients of P_i are 1 in normal situation). However, these parameters have different effects on the proposed model and their intricate relationships render separate analysis complex. Hence, to showcase sensitivity, we assign two distinct coefficients (0.1 & 10) to each parameter, unveiling their impact across all subsystems. Table 7 displays the cumulative changes in new cases, recoveries, and deaths over simulation, underscoring the model's responsiveness.

In the presented model, a set of parameters plays a pivotal role, with seven among them standing out as the most influential. Manipulating these parameters yields diverse impacts on the model's outcomes, a concept exemplified through the subsequent table. Our exploration begins with the initial entry of Table 7, where all parameters hold a coefficient of 0.1. Notably, the inaugural column (P1) exhibits a 0.773 alteration in the summation of daily new cases—an insight into the sway of patients or new cases on demands when assigned a 0.1 coefficient. This underscores the pronounced disparities in parameter effects. Remarkably, the paramount sensitivity lies with P4 (pertaining to private transportation), while P5 (associated with contacts) emerges as a noteworthy influencer of infection dynamics, particularly in the Iranian context.

5.2. Different scenarios and simulation results

This paper presents five scenarios aimed at identifying potential COVID-19 trends within a specific country. The scenarios are as follows:

- Scenario 1: In this scenario, it is assumed that half of the population will maintain their regular routines with slight adjustments due to government-imposed restrictions, while the other half will drastically alter their lifestyles. The government's response involves increasing medical center capacity by 50 %, imposing restrictions on both public and private transportation, and enforcing the closure of numerous businesses.
- Scenario 2: Here, it is assumed that most people will adhere to government regulations while continuing their usual activities with minor alterations prompted by restrictions. The government's measures include expanding medical center capacity, regulating public and private transportation, and closing several businesses.
- Scenario 3: This scenario envisions a complete change in people's daily lives, characterized by strict adherence to announced warnings and a reduction in high-risk behaviors. The government gains control over various situations, manages businesses, and addresses the economic needs of society.
- Scenario 4: Individuals make lifestyle changes, but the government is unable to bolster hospital capacity and supply chains. Consequently, most government actions focus on prevention.
- Scenario 5: Assuming people continue their normal routines and the government remains unable to enhance hospital capacity and supply chains. In this scenario, the government is compelled to reopen 50 % of schools and universities by the end of September 2022 due to the perceived inadequacy of virtual education.

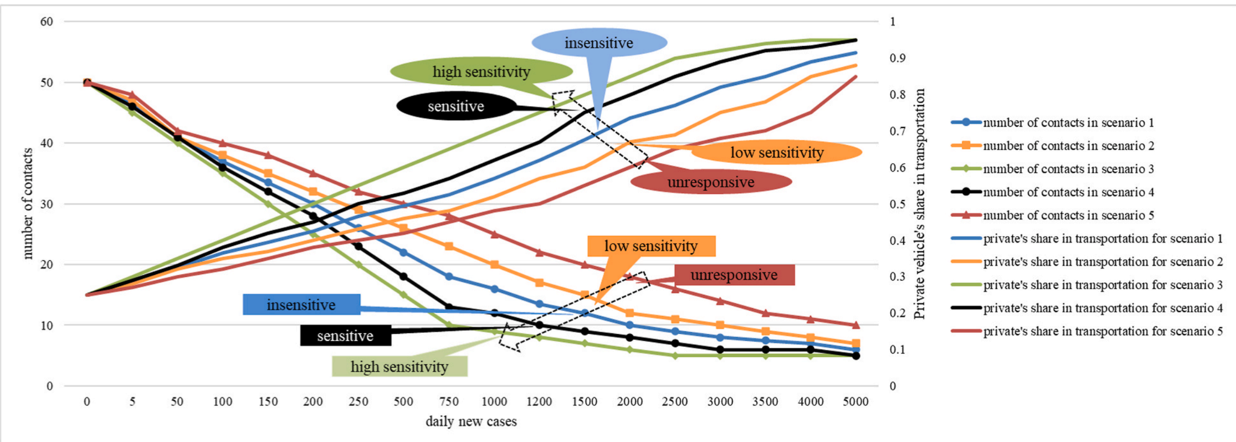

Fig. 12. Number of contacts (left axis) and private vehicle's share in transportation (right or secondary axis) based on different scenarios.

The current discourse among experts in Iran revolves around two alternatives: domestically producing vaccines or importing them from other countries to usher in a new vaccination phase. As such, three distinct situations are identified in conjunction with the aforementioned scenarios:

- o In the first situation, simulated results indicate no new vaccination phase.
- o In the second situation, a new phase of vaccination processes commences from summer (July 2022).
- o In the third situation, a new phase of vaccination processes initiates in fall (October 2022).

Uncertainty is factored into this model through a specified equation. The behavioral dynamics of functional variables differ across scenarios due to societal behaviors. People's responses to daily COVID-19 case counts are categorized as follows:

- ❖ High sensitivity: Individuals are acutely responsive to government warnings, adjusting their behaviors accordingly.
- ❖ Sensitive: People are responsive to government advice, modifying their behaviors as needed.
- ❖ Low sensitivity: Individuals minimally adjust their behaviors in response to government warnings.
- ❖ Insensitive: People do not significantly alter their behaviors despite government advisories.
- ❖ Unresponsive: Individuals continue their routines without heeding government warnings.

To facilitate comprehension, Fig. 12 illustrates changes in contact rates and the proportion of private vehicle usage in transportation relative to daily new case counts. Additional functional variables are presented in Table 8.

Table 8
Classes of different functional forms variables for every scenario.

Subsystem	functional forms variables	Scenario 1	Scenario 2	Scenario 3	Scenario 4	Scenario 5
The spread subsystem	rate of exposed	low sensitivity	insensitive	high sensitivity	sensitive	unresponsive
	rate of infection symptomatically	low sensitivity	insensitive	high sensitivity	sensitive	unresponsive
	rate of infection asymptomatically	low sensitivity	insensitive	high sensitivity	sensitive	unresponsive
	rate of new cases symptomatically	low sensitivity	insensitive	high sensitivity	sensitive	unresponsive
	rate of recovery symptomatically	low sensitivity	insensitive	high sensitivity	sensitive	unresponsive
	rate of recovery asymptomatically	low sensitivity	insensitive	high sensitivity	sensitive	unresponsive
	rate of death symptomatically	low sensitivity	insensitive	high sensitivity	sensitive	unresponsive
	rate of death asymptomatically	low sensitivity	insensitive	high sensitivity	sensitive	unresponsive
The healthcare subsystem	allocated beds for patients of COVID-19	low sensitivity	sensitive	high sensitivity	insensitive	unresponsive
	effect of healthcare centers on recovery	low sensitivity	sensitive	high sensitivity	insensitive	unresponsive
	effect of healthcare centers access	low sensitivity	sensitive	high sensitivity	insensitive	unresponsive
	effect of healthcare centers on mortality	low sensitivity	sensitive	high sensitivity	insensitive	unresponsive
	Vaccination	low sensitivity	sensitive	high sensitivity	insensitive	unresponsive
The transportation subsystem	effects of COVID-19 on private transportation	low sensitivity	insensitive	high sensitivity	sensitive	unresponsive
	transportation for schools	low sensitivity	sensitive	high sensitivity	insensitive	unresponsive
	transportation for universities	low sensitivity	sensitive	high sensitivity	insensitive	unresponsive
The food/drug network subsystem	effect of patients on demands	low sensitivity	insensitive	high sensitivity	sensitive	unresponsive
	effects of shortage on contacts	low sensitivity	sensitive	high sensitivity	insensitive	unresponsive
The contacts subsystem	effect of contacts	low sensitivity	insensitive	high sensitivity	sensitive	unresponsive
	effect of funerals on contacts	low sensitivity	insensitive	high sensitivity	sensitive	unresponsive
	frequency of contacts	low sensitivity	insensitive	high sensitivity	sensitive	unresponsive
	number of contacts	low sensitivity	insensitive	high sensitivity	sensitive	unresponsive

Based on the outcomes of the suggested model, each individual has an estimated average of around 50 contacts in the absence of daily new cases. With an increase in daily new cases, this average number of contacts per person declines. A heightened sensitivity to fluctuations in the daily new case count corresponds to a reduction in daily interactions. Similarly, distinct variables in various scenarios exhibit fitting degrees of sensitivity. Across the range of scenarios, individual responses are most sensitive to the number of daily new cases in scenario 3 and least sensitive in scenario 5.

Fig. 12 and Table 8 provide an overview of the variables encompassing various functional forms within each scenario. These functional variables wield influence over other interconnected variables, operating under distinct active and inactive rules, ultimately culminating in the alteration of final values for the level variables. Table 8 details the functional variables, each assigned specific values in accordance with the scenario-specific assumptions outlined in this case study. In the context of COVID-19 cases, these functional variables are categorized as highly sensitive, sensitive, low sensitivity, insensitive, or unresponsive. Consequently, diverse combinations of these variables are deliberated within each scenario. It's essential to emphasize that sensitivity analyses can serve as a compass for modifying critical variables, thereby yielding results that exhibit reduced losses.

Subsequently, the identified variable constellations are subjected to modeling using the proposed framework to derive pertinent outcomes. This methodology can be extended to examine diverse scenarios, thus illuminating their potential impacts prior to execution. In the third scenario, effective collaboration between the populace and the government leads to the most favorable outcome compared to alternative scenarios. This involves aggregating daily new cases, daily recoveries, daily deaths, and other pertinent factors. Comparable adjustments are made for other relevant parameters, harmonizing them with the unique conditions of each scenario and their respective assumptions. The model is subsequently employed to simulate a span of 1302 days, ranging from February 1, 2020, to August 25, 2023. The outcomes of this simulation are encapsulated in Table 9 and illustrated in Figs. 13–15.

Based on the results, vaccination demonstrates significant effectiveness across all scenarios. Commencing vaccination at the earliest opportunity can further diminish mortality rates within communities. The scenario outcomes underscore that individual behaviors wield the greatest influence on reducing casualties within society. Moreover, the populace's engagement with government initiatives stands out as the subsequent most pivotal factor in casualty reduction. Scenario 3 portrays a society exhibiting heightened sensitivity in behavior and seamless collaboration with governmental measures. After 1302 days of simulation, this scenario registers approximately 3,777,741 new cases and 58,811 deaths. Conversely, Scenario 5 depicts a society characterized by unresponsive behaviors and inadequate government cooperation. In the same 1302-day simulation period, scenario 5 records around 28,837,330 new cases and 436,689 deaths. Notably, the losses incurred in Scenario 5 are nearly 7 times greater than those in Scenario 3.

6. Discussion

Numerous studies have explored various methodologies to simulate infectious diseases in order to model realistic behaviors. As elucidated in the literature review, system dynamics models have gained widespread usage in predicting disease transmission. Therefore, integrating the SEIAR model with a system dynamics approach holds promise for capturing the intricate complexities and sociodynamic factors that influence disease prevalence. This study introduces key innovations, focusing on the incorporation of uncertain variables and diverse effective subsystems into the SEIAR system dynamics framework for respiratory diseases. Additionally, the inclusion of scenario-based and sensitivity analyses enhances the practical applicability of this research in addressing real-world issues. Illustrated through a comprehensive case study of the COVID-19 outbreak, the proposed model effectively demonstrates its advantages. The simulation encompasses daily metrics of new cases, recoveries, and deaths based on predetermined variables. The outcomes, as presented in Table 7, starkly underscore the significant impact of overlooking the influence of public transportation on mortality rates. Conversely, a deliberate focus on transportation yields a noteworthy reduction of 0.702 in daily new cases, whereas inadequate planning amplifies these cases by a staggering factor of 7.774 compared to the current daily rate. Furthermore, negligence in adhering to health protocols during interpersonal contacts can lead to an alarming increase of more than tenfold in the number of infections, exacerbating the daily case count.

The results strongly affirm the efficacy of the proposed system dynamics model, which, rooted in its constituent subsystems, adeptly anticipates a spectrum of scenarios across various parameters. These findings underscore the pivotal role of interactions between individuals and government entities in shaping disease transmission dynamics. Effective governmental policies emerge as pivotal in mitigating costs and losses, while collaboration between citizens and authorities emerges as a potent force in disease control. Moreover, the results emphasize that, while vaccines play a pivotal role in curtailing disease spread, the significance of human reactions and adept governmental management should not be underestimated.

The methodologies presented in this study offer valuable applications beyond COVID-19 for infectious disease impact analysis. For instance, the advanced SEIAR framework with uncertainty mitigation techniques can be adapted to model and manage the spread of emerging respiratory viruses such as influenza strains or novel coronaviruses. The systematic integration of diverse subsystems allows for a nuanced understanding of disease dynamics in various contexts. The model's adaptability makes it applicable to different infectious diseases with varying transmission characteristics. Additionally, the incorporation of real-time data sources and scenario-based analyses can aid in preparing for and mitigating the impact of future pandemics. This versatile approach, grounded in system dynamics, provides a robust foundation for proactive and tailored strategies in the face of diverse infectious disease challenges.

6.1. Managerial, policymakers and theoretical implications

The findings from the sensitivity analysis and the exploration of various scenarios within the presented case study underscore the critical necessity of complete collaboration between the populace and governmental authorities to effectively curb the transmission of

Table 9
Simulated results of defined scenarios in the proposed model.

Results		Total cases after 1302 days of simulation		
		No new phase of vaccine	Vaccine sum2022	Vaccine fall2022
Scenario 1	new cases	7,626,120	4,218,072	6,120,807
	recovered patients	7,387,036	3,843,029	5,745,862
	deaths	147,278	96,478	128,965
Scenario 2	*new cases*	5,611,293	3,014,841	4,258,536
	recovered patients	5,543,041	2,857,877	4,218,142
	deaths	88,198	57,652	77,858
Scenario 3	new cases	3,777,741	1,995,875	2,712,626
	recovered patients	2,788,582	1,557,043	2,229,693
	deaths	58,811	40,497	51,835
Scenario 4	*new cases*	6,760,178	4,016,487	4,973,417
	recovered patients	5,201,543	2,861,876	3,881,449
	deaths	121,529	70,648	91,941
Scenario 5	new cases	28,837,330	14,536,033	20,998,337
	recovered patients	23,354,341	12,230,006	18,233,463
	deaths	436,689	303,151	393,758

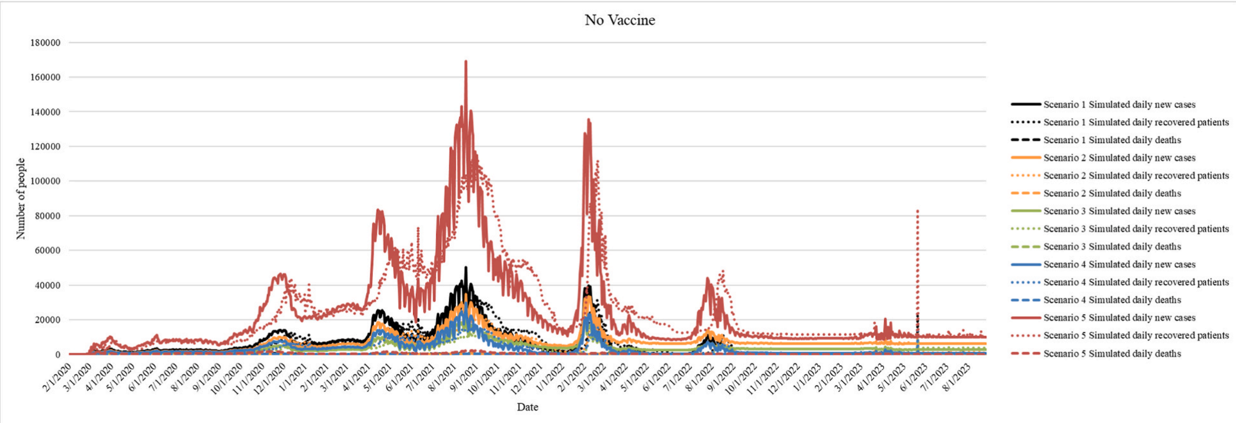

Fig. 13. Simulated results of defined scenarios in the proposed model (no vaccine).

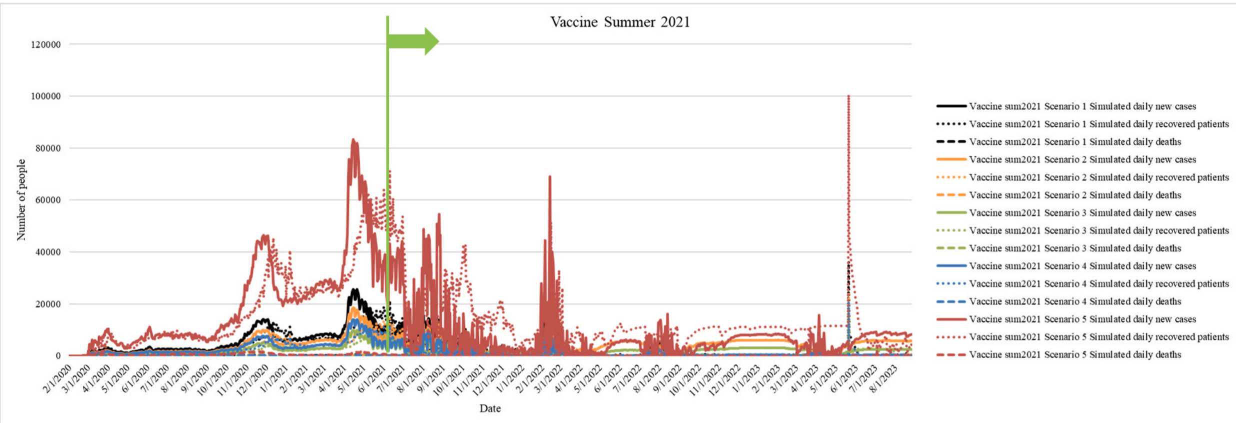

Fig. 14. Simulated results of defined scenarios in the proposed model (vaccine summer 2021).

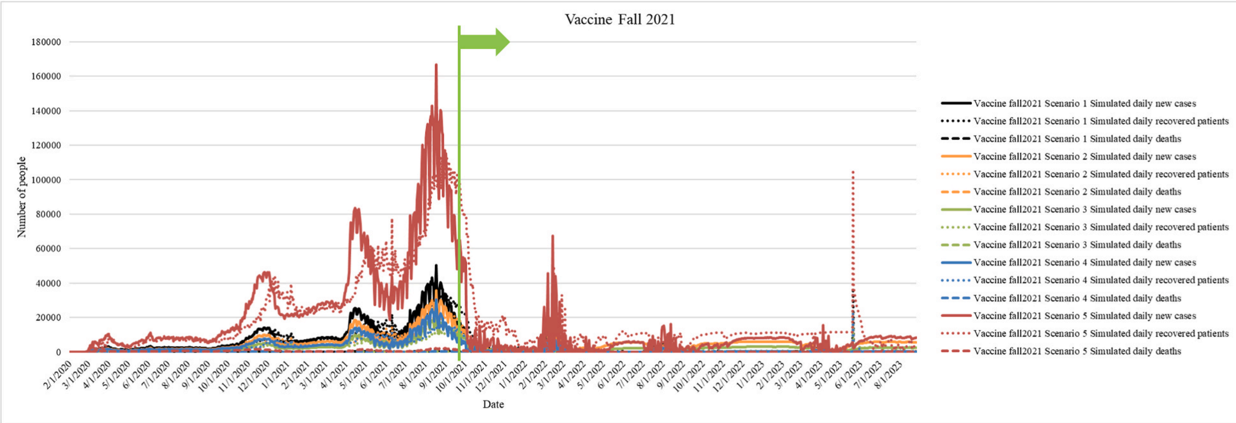

Fig. 15. Simulated results of defined scenarios in the proposed model (vaccine fall 2021).

COVID-19. Referencing Tables 9 and it becomes evident that Scenario 3, involving widespread vaccination, emerges as the most favorable approach, while Scenario 5 represents the least desirable outcome. The outcomes demonstrate that the adoption of either Scenario 5 or Scenario 3 can lead to a range of annual fatalities, spanning from 436,689 to 40,497 respectively.

The implications drawn from the sensitivity analysis robustly advocate for stringent control measures for human interactions and transportation. In this context, it is imperative for governments to establish the requisite infrastructure that mitigates disturbances to individuals' daily routines. Moreover, the resumption of communal facilities such as sports clubs, schools, and universities carries the inherent risk of precipitating unmanageable circumstances. As a countermeasure, advocating for virtual education and solitary forms of entertainment within the community aligns with prudent managerial and policymaking strategies.

Additionally, the reinforcement of healthcare systems demands significant governmental support. Containing the propagation of COVID-19 mandates the allocation of dedicated healthcare centers to treat afflicted patients, alongside ensuring continued services for other medical needs so as to safeguard overall quality of life. Although the existing infrastructure in Iran adequately addresses concerns related to food and pharmaceutical distribution, these subsystems should not be disregarded, given their potential impact on the virus's transmission dynamics.

Moreover, the efficacy of vaccination emerges as a consistent factor across all scenarios. Notably, in Scenario 3 where the synergy between the populace and government is most pronounced, the potency of vaccination surpasses that observed in other scenarios. This underscores the imperative of meticulous vaccination planning and execution, further highlighting its pivotal role in pandemic management.

7. Conclusion

In summary, this study addresses the critical challenge posed by respiratory viruses, recognizing them as a significant global health threat. The complex interplay of factors influencing respiratory diseases necessitates the use of simulations and predictive analyses to formulate effective containment strategies. Understanding the multifaceted nature of systems and subsystems governing disease transmission is crucial, prompting the development of a comprehensive system dynamics model.

Our proposed model, rooted in the SEIAR framework and incorporating five essential subsystems—spread dynamics, healthcare infrastructure, transportation networks, food and drug distribution channels, and social contacts—offers a robust tool for assessing potential outbreak scenarios. Through an in-depth examination focused on COVID-19 in Iran, the model's efficacy is demonstrated across five diverse scenarios, providing valuable insights into the dynamics of disease transmission.

Iran, as the 19th nation grappling with COVID-19, faces unique challenges influenced by international constraints. The study utilizes Iran's context to showcase the model's utility, supported by sensitivity analyses encompassing various parameters. The exploration spans five scenarios, evaluating crucial metrics during Iran's outbreak: daily new cases, daily fatalities, and daily recoveries. Notably, the model incorporates the impact of vaccination, revealing key revelations that inform effective disease management strategies. The study highlights the pivotal role of vaccination campaigns and collaborative governance in reducing fatalities. The model's proficiency in identifying vulnerable populations and optimizing immunization strategies demonstrates its effectiveness in managing successive waves of contagion. Transportation and interpersonal contacts emerge as critical variables driving disease proliferation in the context of COVID-19 in Iran.

To assess the model's performance, we employ the NRMSD, revealing impressively low values of 0.2 % for daily new cases, 1.2 % for daily fatalities, and 0.6 % for daily recoveries when compared to real-world data. This attests to the model's robustness, with an average error of less than 2 %. Looking ahead, the model holds promise for broader applications in other countries, offering adaptability to accommodate unique subsystems based on each nation's context. The key findings underscore the importance of timely and widespread vaccination in curbing disease spread, with the potential to significantly reduce mortality rates. Collaborative governance emerges as a powerful force in effective disease control, emphasizing the need for cohesive efforts between citizens and authorities.

The study sheds light on the intricate dynamics of disease transmission, revealing the substantial impact of transportation and interpersonal contacts on the proliferation of respiratory viruses.

In conclusion, this research contributes a valuable framework for anticipating and managing respiratory virus diseases. By offering a comprehensive system dynamics model, we provide a tool that not only addresses the challenges posed by COVID-19 in Iran but also holds broader applicability for global health management. The study's insights have significant implications for policymakers, healthcare professionals, and researchers engaged in the ongoing battle against respiratory virus diseases, emphasizing the importance of a holistic and collaborative approach to disease control.

7.1. Limitations or challenges

While our study offers a promising model for respiratory virus dynamics, it acknowledges key limitations. The model's effectiveness relies on precise input parameters, which are susceptible to uncertainties in rapidly evolving pandemics. Future research should prioritize refining parameters with updated data. Societal behavior complexity poses a challenge, as our model simplifies human interactions and compliance dynamics. Incorporating nuanced social factors could enhance realism. The study primarily focuses on COVID-19 in Iran, requiring careful validation for generalizability. Unique regional characteristics demand adaptation. The model assumes a constant environment, neglecting external shocks. Adapting to dynamic external factors could boost predictive capabilities. Acknowledging these limitations emphasizes areas for refinement, underscoring ongoing research needs for broader accuracy across diverse scenarios and regions.

7.2. Future research

Future research should enhance the model's applicability by investigating its adaptability across diverse global contexts and assessing performance in countries with varying healthcare systems, demographics, and socio-economic factors. Integrating real-time data sources and advanced machine learning can boost predictive capabilities by incorporating information on population mobility, vaccination rates, and virus mutations. Exploring the model's robustness under different epidemic scenarios, refining parameters based on scientific understanding, and involving interdisciplinary collaboration will strengthen its versatility. The focus should be on validating and extending the model's utility, integrating real-time data, exploring robustness, refining parameters, and fostering interdisciplinary collaboration for a holistic understanding of respiratory virus dynamics globally.

Data availability statement

Data and models will be made available on request (contact authors: ershadi.mm1372@aut.ac.ir and zeinab.rahimi@aut.ac.ir).

CRediT authorship contribution statement

Mohammad Mahdi Ershadi: Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Software, Resources, Project administration, Methodology, Formal analysis, Data curation, Conceptualization. **Zeinab Rahimi Rise:** Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Resources, Project administration, Methodology, Formal analysis, Data curation, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

[1] Zhongbao Zuo, et al., Trends in respiratory diseases before and after the COVID-19 pandemic in China from 2010 to 2021, BMC Publ. Health 23 (1) (2023) 1–11, https://doi.org/10.1186/s12889-023-15081-4.

[2] Ziwei Cui, et al., Forecasting the transmission trends of respiratory infectious diseases with an exposure-risk-based model at the microscopic level, Environ. Res. 212 (2022) 113428, https://doi.org/10.1016/j.envres.2022.113428.

[3] Hongju Guo, et al., Time series study on the effects of daily average temperature on the mortality from respiratory diseases and circulatory diseases: a case study in Mianyang City, BMC Publ. Health 22 (1) (2022) 1001, https://doi.org/10.1186/s12889-022-13384-6.

[4] Zuiyuan Guo, et al., Dynamic model of respiratory infectious disease transmission in urban public transportation systems, Heliyon 9 (3) (2023), https://doi.org/10.1016/j.heliyon.2023.e14500.

[5] J.C. Arias, M.I. Ramos, J.J. Cubillas, Predicting emergency health care demands due to respiratory diseases, Int. J. Med. Inf. 177 (2023) 105163, https://doi.org/10.1016/j.ijmedinf.2023.105163.

[6] Beyda Tasar, Orhan Yaman, Turker Tuncer, Accurate respiratory sound classification model based on piccolo pattern, Appl. Acoust. 188 (2022) 108589, https://doi.org/10.1016/j.apacoust.2021.108589.

[7] Juuso Jalasto, et al., Occupation, socioeconomic status and chronic obstructive respiratory diseases–The EpiLung study in Finland, Estonia and Sweden, Respir. Med. 191 (2022) 106403, https://doi.org/10.1016/j.rmed.2021.106403.

[8] Anne Bernadou, et al., Estimating the burden of influenza-attributable severe acute respiratory infections on the hospital system in Metropolitan France, 2012–2018, BMC Infect. Dis. 23 (1) (2023) 128. https://link.springer.com/article/10.1186/s12879-023-08078-2.

[9] Sha He, et al., Modelling optimal control of air pollution to reduce respiratory diseases, Appl. Math. Comput. 458 (2023) 128223, https://doi.org/10.1016/j.amc.2023.128223.

[10] Eduardo L. Krüger, Spohr Nedel Anderson, Investigating the relationship between climate and hospital admissions for respiratory diseases before and during the COVID-19 pandemic in Brazil, Sustainability 15 (1) (2022) 288, https://doi.org/10.3390/su15010288.
[11] Lei Shi, Longxing Qi, Dynamic analysis and optimal control of a class of SISP respiratory diseases, J. Biol. Dynam. 16 (1) (2022) 64–97, https://doi.org/10.1080/17513758.2022.2027529.
[12] Björn Goldenbogen, et al., Control of COVID-19 outbreaks under stochastic community dynamics, bimodality, or limited vaccination, Adv. Sci. 9 (23) (2022) 2200088, https://doi.org/10.1002/advs.202200088.
[13] Lei Shi, Longxing Qi, Bin Ding, Bifurcation analysis of a respiratory disease model about air pollution direct and indirect effects, Math. Methods Appl. Sci. 46 (5) (2023) 6210–6244, https://doi.org/10.1002/mma.8900.
[14] Ting Dang, et al., Exploring longitudinal cough, breath, and voice data for COVID-19 progression prediction via sequential deep learning: model development and validation, J. Med. Internet Res. 24 (6) (2022) e37004. https://www.jmir.org/2022/6/e37004/.
[15] Shuxuan Song, et al., From outbreak to near disappearance: how did non-pharmaceutical interventions against Covid-19 affect the transmission of influenza virus? Front. Public Health 10 (2022) 863522 https://doi.org/10.3389/fpubh.2022.863522.
[16] Casey F. Breen, Ayesha S. Mahmud, Dennis M. Feehan, Novel estimates reveal subnational heterogeneities in disease-relevant contact patterns in the United States, PLoS Comput. Biol. 18 (12) (2022) e1010742, https://doi.org/10.1371/journal.pcbi.1010742.
[17] Martina Fazio, et al., Exploring the impact of mobility restrictions on the COVID-19 spreading through an agent-based approach, J. Transport Health 25 (2022) 101373, https://doi.org/10.1016/j.jth.2022.101373.
[18] Notice Ringa, et al., Social contacts and transmission of COVID-19 in British Columbia, Canada, Front. Public Health 10 (2022) 867425, https://doi.org/10.3389/fpubh.2022.867425.
[19] Lifen Jia, Wei Chen, Uncertain SEIAR model for COVID-19 cases in China, Fuzzy Optim. Decis. Making 20 (2021) 243–259, https://doi.org/10.1007/s10700-020-09341-w.
[20] Lenka Pribylová, Veronika Hajnova, SEIAR Model with Asymptomatic Cohort and Consequences to Efficiency of Quarantine Government Measures in COVID-19 Epidemic, 2020, https://doi.org/10.48550/arXiv.2004.02601 arXiv preprint arXiv:2004.02601.
[21] Min Chen, et al., The introduction of population migration to SEIAR for COVID-19 epidemic modeling with an efficient intervention strategy, Inf. Fusion 64 (2020) 252–258, https://doi.org/10.1016/j.inffus.2020.08.002.
[22] Xinwu Qian, Satish V. Ukkusuri, Connecting urban transportation systems with the spread of infectious diseases: a Trans-SEIR modeling approach, Transp. Res. Part B Methodol. 145 (2021) 185–211, https://doi.org/10.1016/j.trb.2021.01.008.
[23] Sadat Asl, Akbar Ali, et al., Fuzzy expert systems for prediction of ICU admission in patients with COVID-19, Intell. Decis. Technol. 16 (1) (2022) 159–168, https://doi.org/10.3233/IDT-200220.
[24] Borwornsom Leerapan, et al., System dynamics modelling of health workforce planning to address future challenges of Thailand's Universal Health Coverage, Hum. Resour. Health 19 (1) (2021) 1–16, https://doi.org/10.1186/s12960-021-00572-5.
[25] Mohammad Mahdi Ershadi, Hossein Shams Shemirani, Using mathematical modeling for analysis of the impact of client choice on preventive healthcare facility network design, Int. J. Healthc. Manag. 14 (2) (2021) 588–602, https://doi.org/10.1080/20479700.2019.1679518.
[26] Jeanne M. Fair, et al., Systems dynamics and the uncertainties of diagnostics, testing and contact tracing for COVID-19, Methods 195 (2021) 77–91, https://doi.org/10.1016/j.ymeth.2021.03.008.
[27] Heting Zhang, et al., Optimal control strategies for a two-group epidemic model with vaccination-resource constraints, Appl. Math. Comput. 371 (2020) 124956, https://doi.org/10.1016/j.amc.2019.124956.
[28] David M. Rubin, et al., Facilitating understanding, modeling and simulation of infectious disease epidemics in the age of COVID-19, Front. Public Health 9 (2021) 593417, https://doi.org/10.3389/fpubh.2021.593417.
[29] Fahimeh Allahi, et al., The COVID-19 epidemic and evaluating the corresponding responses to crisis management in refugees: a system dynamic approach, J. Humanit. Logist. Supply Chain Manag. 11 (2) (2021) 347–366, https://doi.org/10.1108/JHLSCM-09-2020-0077.
[30] Shuwei Jia, Li Yao, Tianhui Fang, System dynamics analysis of COVID-19 prevention and control strategies, Environ. Sci. Pollut. Control Ser. 29 (2022) 3944–3957, https://doi.org/10.1007/s11356-021-15902-2.
[31] Bo Hu, et al., Analysis of the real number of infected people by COVID-19: a system dynamics approach, PLoS One 16 (3) (2021) e0245728, https://doi.org/10.1371/journal.pone.0245728.
[32] Yunfei Gu, et al., Small Island Developing States (SIDS) COVID-19 post-pandemic tourism recovery: a system dynamics approach, Curr. Issues Tourism 25 (9) (2022) 1481–1508, https://doi.org/10.1080/13683500.2021.1924636.
[33] Charlle Sy, et al., Policy development for pandemic response using system dynamics: a case study on COVID-19, Process Integration and Optimization for Sustainability 4 (2020) 497–501, https://doi.org/10.1007/s41660-020-00130-x.
[34] Erman Aminullah, Erwiza Erman, Policy innovation and emergence of innovative health technology: the system dynamics modelling of early COVID-19 handling in Indonesia, Technol. Soc. 66 (2021) 101682, https://doi.org/10.1016/j.techsoc.2021.101682.
[35] Oscar Castillo, Patricia Melin, A new fuzzy fractal control approach of non-linear dynamic systems: the case of controlling the COVID-19 pandemics, Chaos, Solit. Fractals 151 (2021) 111250, https://doi.org/10.1016/j.chaos.2021.111250.
[36] Rahimi Rise, Zeynab Mohammad Mehdi Ershadi, Seyed Hamidreza Shahabi Haghighgi, Scenario-based analysis about COVID-19 outbreak in Iran using systematic dynamics modeling-with a focus on the transportation system, Journal of Transportation Research 17 (2) (2020) 33–48. https://dorl.net/dor/20.1001.1.17353459.1399.17.2.3.2.
[37] Zeinab Rahimi Rise, Mohammad Mahdi Ershadi, Socioeconomic analysis of infectious diseases based on different scenarios using uncertain SEIAR system dynamics with effective subsystems and ANFIS, Journal of Economic and Administrative Sciences ahead-of-print (2022), https://doi.org/10.1108/JEAS-07-2021-0124.
[38] Rahimi Rise, Zeinab Mohammad Mahdi Ershadi, Mohammad Javad Ershadi, Multidisciplinary analysis of international environments based on impacts of Covid-19: state of art, International Journal of Industrial Engineering & Production Research 33 (1) (2022) 1–10, https://doi.org/10.22068/ijiepr.33.1.14.
[39] Mohammad Mahdi Ershadi, Hossein Shams Shemirani, A multi-objective optimization model for logistic planning in the crisis response phase, J. Humanit. Logist. Supply Chain Manag. 12 (1) (2022) 30–53, https://doi.org/10.1108/JHLSCM-11-2020-0108.
[40] Yajie Zhu, et al., Effectiveness analysis of multiple epidemic prevention measures in the context of COVID-19 using the SVIRD model and ensemble Kalman filter, Heliyon 9 (3) (2023), https://doi.org/10.1016/j.heliyon.2023.e14231.

Mohammad Mahdi Ershadi obtained his BSc in Industrial Engineering from Isfahan University of Technology in 2015. In 2017, he completed his MSc in Industrial Engineering from Amirkabir University of Technology. Since 2017, he has been an active researcher at Amirkabir University of Technology. His research pursuits span across data engineering, operations research, and healthcare systems. WoS: https://www.webofscience.com/wos/author/record/1047849 Google Scholar: https://scholar.google.com/citations?user=YDqbCaMAAAAJ&hl=en&oi=ao. ORCID: https://orcid.org/0000-0002-7409-6469 Email: ershadi.mm1372@aut.ac.ir; Address: No. 350, Hafez Ave, Valiasr Square, Tehran, Iran, 1591634311, Amirkabir University of Technology. Contributions of Mohammad Mahdi Ershadi: (1) the conception and design of the study, the acquisition of data, and the analysis and interpretation of data; (2) drafting the article and critically revising its important intellectual content; (3) final approval of the version submitted.

Zeinab Rahimi Rise earned her degree in Industrial Engineering from Ershad-Damavand University in 2014, and she completed her master's in Industrial Engineering from Amirkabir University of Technology in 2018. Her areas of fascination in research encompass machine learning, image processing, and healthcare systems. ORCID: https://orcid.org/0000-0001-6146-6590 Email: zeinab.rahimi@aut.ac.ir; Address: No. 350, Hafez Ave, Valiasr Square, Tehran, Iran, 1591634311, Amirkabir University of Technology. Contributions of Zeinab Rahimi Rise: (1) the conception and design of the study, the acquisition of data, and the analysis and interpretation of data; (2) drafting the article and critically revising its important intellectual content; (3) final approval of the version submitted.